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Gencore version 4.5  
P08476 homo sapien  
P18075 homo sapien  
P55103 homo sapien  
P43029 mus musculus  
P23359 mus musculus  
P43027 mus musculus  
P43026 homo sapien  
P34820 homo sapien  
P08717 mus musculus  
08859 rattus norvegicus  
09wuk5 rattus norvegicus  
P92172 caenorhabditis elegans

OM protein - protein search, using sw model

Run on: May 20, 2002, 09:21:15 ; Search time 11.88 Seconds

(without alignments)  
355.255 Million cell updates/sec

Title: Perfect score: US-09-754-826-2

Sequence: 1 DFGIDCDEHSTESRCRYPL..... KEQITYGK1PAMVVDRCCGS 109

Scoring table: BLOSUM62

Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : swissprot\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	622	99.0	375	1 GDF8_CHICK	04220 gallus gallus
2	622	99.0	375	1 GDF8_HUMAN	01493 homo sapien
3	622	99.0	375	1 GDF8_MELGA	04221 meleagris gallicus
4	622	99.0	375	1 GDF8_MOUSE	018931 sus scrofa
5	622	99.0	376	1 GDF8_RAT	008899 mus musculus
6	622	99.0	376	1 GDF8_PAPTA	035312 rattus norvegicus
7	615	98.1	375	1 GDF8_SHEEP	018828 ovis aries
8	612	97.5	375	1 GDF8_BOVINE	018830 bos taurus
9	611	97.3	375	1 GDF8_PIG	018834 sus scrofa
10	574	91.4	405	1 GDFB_HUMAN	095390 homo sapien
11	563	89.6	374	1 GDFB_BRADY	042222 brachyury
12	563	89.6	345	1 GDFB_RAT	092217 rattus norvegicus
13	241	38.4	255	1 IHBB_MOUSE	042219 mus musculus
14	239	38.1	355	1 DVRL_BRARE	P35221 brachyury
15	235	37.6	391	1 IHBB_CHICK	P27995 gallus gallus
16	235	37.4	349	1 IHBB_PIG	P04088 sus scrofa
17	235	37.4	407	1 IHBB_HUMAN	P09229 homo sapien
18	235	37.4	408	1 IHBB_BOVINE	P42017 bos taurus
19	235	37.4	207	1 BMP6_RAT	Q44999 rattus norvegicus
20	225.5	35.9	513	1 BMP6_HUMAN	P22004 homo sapien
21	225.5	35.9	510	1 BMP6_MOUSE	P20722 mus musculus
22	223.5	35.5	426	1 IHBA_HORSE	P55022 equus caballus
23	216.5	34.5	360	1 DVRL_XENLA	P09334 xenopus laevis
24	212.5	33.8	125	1 GDF6_MOUSE	P43028 mus musculus
25	211.5	33.7	352	1 IHBC_MOUSE	P55104 mus musculus
26	211.5	33.7	436	1 GDF6_BOVINE	P55106 bos taurus
27	211.5	33.5	424	1 IHBA_MOUSE	Q04998 mus musculus
28	210.5	33.5	424	1 IHBA_PIG	P03970 sus scrofa
29	210.5	33.5	424	1 IHBA_RAT	P18331 rattus norvegicus
30	210.5	33.5	425	1 IHBA_BOVINE	P07995 bos taurus
31	210.5	33.5	425	1 IHBA_SHEEP	P43032 ovis aries
32	210.5	33.5	426	1 BMP7_XENLA	P30886 xenopus laevis
33	210.5	33.5			

#### ALIGNMENTS

RESULT	1	GDF8_CHICK	STANDARD:	PRT:	375 AA.
ID	GDF8_CHICK				
AC	042220;	DT	15-JUL-1999 (Rel. 38, Created)		
CC		DT	15-JUL-1999 (Rel. 38, Last sequence update)		
CC		DT	16-OCT-2001 (Rel. 40, Last annotation update)		
CC		DE	Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).		
CC		GN	GDF8 OR MSTN.		
CC		OS	Galulus gallus (Chicken)		
CC		OC	Bukarivota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus		
CC		OC			
CC		OX			
CC		RN			
CC		RR			
CC		RC			
CC		RX			
CC		RA			
CC		MCPI			
CC		RT			
CC		RL			
CC		PRO			
CC		NCB1_TAXID=9031;			
CC		[1]			
CC		SEQUENCE FROM N.A.			
CC		STRAIN=WHITE LEJHORN; TISSUE=Skeletal muscle;			
CC		MEDLINE=98024153; PubMed=9356471;			
CC		RA			
CC		MCPI			
CC		RN			
CC		RR			
CC		RC			
CC		RX			
CC		RA			
CC		MCPI			
CC		RT			
CC		RL			
CC		PRO			
CC		NCB1_TAXID=9031;			
CC		[1]			
CC		SEQUENCE FROM N.A.			
CC		STRAIN=WHITE LEJHORN; TISSUE=Skeletal muscle;			
CC		MEDLINE=98024153; PubMed=9356471;			
CC		RA			
CC		MCPI			
CC		RN			
CC		RR			
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CC		RX			
CC		RA			
CC		MCPI			
CC		RT			
CC		RL			
CC		PRO			
CC		NCB1_TAXID=9031;			
CC		[1]			
CC		SEQUENCE FROM N.A.			
CC		STRAIN=WHITE LEJHORN; TISSUE=Skeletal muscle;			
CC		MEDLINE=98024153; PubMed=9356471;			
CC		RA			
CC		MCPI			
CC		RT			
CC		RL			
CC		PRO			
CC		NCB1_TAXID=9031;			
CC		[1]			
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CC		STRAIN=WHITE LEJHORN; TISSUE=Skeletal muscle;			
CC		MEDLINE=98024153; PubMed=9356471;			
CC		RA			
CC		MCPI			
CC		RT			
CC		RL			
CC		PRO			
CC		NCB1_TAXID=9031;			
CC		[1]			
CC		SEQUENCE FROM N.A.			
CC		STRAIN=WHITE LEJHORN; TISSUE=Skeletal muscle;			
CC		MEDLINE=98024153; PubMed=9356471;			
CC		RA			
CC		MCPI			
CC		RT			
CC		RL			
CC		PRO			
CC		NCB1_TAXID=9031;			
CC		[1]			
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CC		STRAIN=WHITE LEJHORN; TISSUE=Skeletal muscle;			
CC		MEDLINE=98024153; PubMed=9356471;			
CC		RA			
CC		MCPI			
CC		RT			
CC		RL			
CC		PRO			
CC		NCB1_TAXID=9031;			
CC		[1]			
CC		SEQUENCE FROM N.A.			
CC		STRAIN=WHITE LEJHORN; TISSUE=Skeletal muscle;			
CC		MEDLINE=98024153; PubMed=9356471;			
CC		RA			
CC		MCPI			
CC		RT			
CC		RL			
CC		PRO			
CC		NCB1_TAXID=9031;			
CC		[1]			
CC		SEQUENCE FROM N.A.			
CC		STRAIN=WHITE LEJHORN; TISSUE=Skeletal muscle;			
CC		MEDLINE=98024153; PubMed=9356471;			
CC		RA			
CC		MCPI			
CC		RT			
CC		RL			
CC		PRO			
CC		NCB1_TAXID=9031;			
CC		[1]			
CC		SEQUENCE FROM N.A.			
CC		STRAIN=WHITE LEJHORN; TISSUE=Skeletal muscle;			
CC		MEDLINE=98024153; PubMed=9356471;			
CC		RA			
CC		MCPI			
CC		RT			
CC		RL			
CC		PRO			
CC		NCB1_TAXID=9031;			
CC		[1]			
CC		SEQUENCE FROM N.A.			
CC		STRAIN=WHITE LEJHORN; TISSUE=Skeletal muscle;			
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CC		RA			
CC		MCPI			
CC		RT			
CC		RL			
CC		PRO			
CC		NCB1_TAXID=9031;			
CC		[1]			
CC		SEQUENCE FROM N.A.			
CC		STRAIN=WHITE LEJHORN; TISSUE=Skeletal muscle;			
CC		MEDLINE=98024153; PubMed=9356471;			
CC		RA			
CC		MCPI			
CC		RT			
CC		RL			
CC		PRO			
CC		NCB1_TAXID=9031;			
CC		[1]			
CC		SEQUENCE FROM N.A.			
CC		STRAIN=WHITE LEJHORN; TISSUE=Skeletal muscle;			
CC		MEDLINE=98024153; PubMed=9356471;			
CC		RA			
CC		MCPI			
CC		RT			
CC		RL			
CC		PRO			
CC		NCB1_TAXID=9031;			
CC		[1]			
CC		SEQUENCE FROM N.A.			
CC		STRAIN=WHITE LEJHORN; TISSUE=Skeletal muscle;			
CC		MEDLINE=98024153; PubMed=9356471;			
CC		RA			
CC		MCPI			
CC		RT			
CC		RL			
CC		PRO			
CC		NCB1_TAXID=9031;			
CC		[1]			
CC		SEQUENCE FROM N.A.			
CC		STRAIN=WHITE LEJHORN; TISSUE=Skeletal muscle;			
CC		MEDLINE=98024153; PubMed=9356471;			
CC		RA			
CC		MCPI			
CC		RT			
CC		RL			
CC		PRO			
CC		NCB1_TAXID=9031;			
CC		[1]			
CC		SEQUENCE FROM N.A.			
CC		STRAIN=WHITE LEJHORN; TISSUE=Skeletal muscle;			
CC		MEDLINE=98024153; PubMed=9356471;			
CC		RA			
CC		MCPI			
CC		RT			
CC		RL			
CC		PRO			
CC		NCB1_TAXID=9031;			
CC		[1]			
CC		SEQUENCE FROM N.A.			
CC		STRAIN=WHITE LEJHORN; TISSUE=Skeletal muscle;			
CC		MEDLINE=98024153; PubMed=9356471;			
CC		RA			
CC		MCPI			
CC		RT			
CC		RL			
CC		PRO			
CC		NCB1_TAXID=9031;			
CC		[1]			
CC		SEQUENCE FROM N.A.			
CC		STRAIN=WHITE LEJHORN; TISSUE=Skeletal muscle;			
CC		MEDLINE=98024153; PubMed=9356471;			
CC		RA			
CC		MCPI			
CC		RT			
CC		RL			
CC		PRO			
CC		NCB1_TAXID=9031;			
CC		[1]			
CC		SEQUENCE FROM N.A.			
CC		STRAIN=WHITE LEJHORN; TISSUE=Skeletal muscle;			
CC		MEDLINE=980241			

Best Local Similarity 99.1%;	Pred. No. 4e-63;	Matches 108;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
OY	1	DRLGLDCEHESFRCCRYPLTVDFEAGWDMIIAPRYKANYCSGCECFVLOQYKPHL	60			
Db	267	DRLGLDCEHESFRCCRYPLTVDFEAGWDMIIAPRYKANYCSGCECFVLOQYKPHL	326			
QY	61	VHQANPRGSAGPCCPTPLMSPINMLYFNKGKQIYKIPAMVDRGCS	109			
Db	327	VHQANPRGSAGPCCPTPLMSPINMLYFNKGKQIYKIPAMVDRGCS	375			
RESULT 2						
ID GDF8_HUMAN		STANDARD;	PRT;	375 AA.		
AC 014793;						
DT 15-JUL-1999 (Rel. 38, Created)						
DT 15-JUL-1999 (Rel. 38, Last sequence update)						
DT 01-MAR-2002 (Rel. 41, Last annotation update)						
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).						
GN GDF8 OR MSTN.						
OS Homo sapiens (Human).						
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
OX NCBI_TaxID=9606;						
RP						
RC TISSUE=Skeletal muscle;						
RA McPherson A.C., Lee S.-J.;						
RT "Double muscling in cattle due to mutations in the myostatin gene.";						
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).						
RN [1]						
RP SEQUENCE FROM N.A.						
RC TISSUE=Muscle;						
RA MEDLINE=99061197; PUBMED=9843994;						
RA Gonzalez-Cadavid N.F., Taylor W.E., Yarasheski K., Sinha-Hikim I.,						
RA Ma K., Ezzat S., Shen R., Lalani R., Asa S., Mamita M., Nair G.,						
RA Arver S., Bhasin S.,						
RT "Organization of the human myostatin gene and expression in healthy men and HIV-infected men with muscle wasting.";						
RT Proc. Natl. Acad. Sci. U.S.A. 95:14938-14943(1998).						
CC -i- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL						
CC MUSCLE GROWTH.						
CC -i- SUBUNIT: HOMODIMER: DISULFIDE-LINKED (BY SIMILARITY).						
CC -i- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.						
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CC EMBL; AF019627; AAB86694.1; -;						
CC EMBL; AF104922; AAC96327.1; -;						
CC HSSP; P18075; IBM.						
CC MIM: 601788; -;						
CC InterPro; IPR001839; TGF-beta.						
CC DR InterPro; IPR00111; TGFb_N.						
CC DR InterPro; IPR00111; TGFb.						
CC DR Pfam; PF00019; TGF-beta; 1.						
CC DR Pfam; PF00088; TGFb_propeptide; 1.						
CC DR PRODOM; P000357; TGF-beta; 1.						
CC DR SMART; SM00204; TGFb; 1.						
CC DR PROSITE; PS00250; TGF_BETA_1; 1.						
CC DR PROSITE; PS00250; TGF_BETA_1.						
CC KW Growth factor; Cytokine; Glycoprotein; Signal.						
CC FT SIGNAL 1 23 POTENTIAL.						
CC FT PROPEP 24 266 POTENTIAL.						
CC FT CHAIN 267 375 GROWTH/DIFFERENTIATION FACTOR 8.						
CC FT DISULFID 281 340 BY SIMILARITY.						
CC FT DISULFID 309 372 BY SIMILARITY.						
CC FT DISULFID 313 374 BY SIMILARITY.						
FT DISULFID 339 339 INTERCHAIN (BY SIMILARITY).						
FT CARBOHYD 71 71 N-LINKED (GICNAC, -) (POTENTIAL).						
FT SEQUENCE 375 AA; 42750 MW; D2AEB732AE84E77 CRC64;						
Query Match 99.0% Score 622; DB 1; Length 375;						

Best Local Similarity 99.1%; Pred. No. 4e-63; Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0; OY 1 DFGLCDDEHISTEESRCRCRYPLTVDFEAFCWDWIAPKRYKANICSGCECBVFQKYPTHL 60

Db 267 DFGLCDDEHISTEESRCRCRYPLTVDFEAFCWDWIAPKRYKANICSGCECBVFQKYPTHL 326

OY 61 VHOANPRGSAGPCCTPTMSPTINMLYFNGKEQIYKGKIPAMVDRCCS 109

Db 327 VHOANPRGSAGPCCTPTMSPTINMLYFNGKEQIYKGKIPAMVDRCCS 375

RESULT 4

ID GDF8\_PIG STANDARD: PRT; 375 AA.

AC 018831; 018831; Lee S.-J.;

DT 15-JUL-1999 (Rel. 38, Created)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

GT Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).

GN GDF8 OR MSTN.

OS Sus scrofa (Pig).

OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OX NCBI\_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Skeletal muscle;

RX MEDLINE-9824153; PubMed-9356471;

RA McPherron A.C.; Lee S.-J.;

RT "Double muscling in cattle due to mutations in the myostatin gene.;"

RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=DUROC, HAMPSHIRE, MEISHAN, AND YORKSHIRE;

RC TISSUE=Skeletal muscle;

RA Voelker G.R.; Conroy J.C.; Wheeler M.B.;

RT Porcine myostatin cDNA sequences: Duroc, Hampshire, Meishan and Yorkshire pigs.;

RL Submitted (sep-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE OF 1-10 AND 36-375 FROM N.A.

RC TISSUE=Muscle;

RA Daneau I. ' Silverides D.W.;

RL Submitted (sep-1998) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL MUSCLE GROWTH.

CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC

EMBL; AP019633; AAC86590; 1; -

DR EMBL; AF188635; AF02770; 1; -

DR EMBL; AF188636; AF02771; 1; -

DR EMBL; AF188637; AF02772; 1; -

DR EMBL; AF188638; AF02773; 1; -

DR EMBL; AF033855; AAC08035; 1; -

DR EMBL; AP093798; AAC62489; 1; -

DR HSSP; P18075; 1BMP.

DR InterPro; IPK00111; TGFb\_N.

DR Pfam; PF00019; TGF-beta; 1.

DR Pfam; PF00688; TGFb\_propeptide; 1.

DR Pfam; PF000357; TGF-beta; 1.

DR SMART; SM00204; TGFb; 1.

DR PROSITE; PS00250; TGF-BETA\_1; 1.

RESULT 5

ID GDF8\_MOUSE STANDARD: PRT; 376 AA.

AC 008689; 008689;

DT 01-NOV-1997 (Rel. 35, Created)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

GT Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).

GN GDF8 OR MSTN

OS Mus musculus (Mouse).

OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CD-1; TISSUE=Skeletal muscle;

RA McPherron A.C.; Lawler A.M.; Lee S.-J.;

RT "Regulation of skeletal muscle mass in mice by a new TGF-beta superfamily member.;"

RL Nature 387:83-90(1997).

CC -!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL MUSCLE GROWTH.

CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).

CC -!- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN DEVELOPING AND ADULT SKELETAL MUSCLE. WRK EXPRESSION IN ADIPOSE TISSUE.

CC -!- DEVELOPMENTAL STAGE: FIRST DETECTED AT DAY 9.5 POST-COITUM IN ONE-THIRD OF DEVELOPING SOMITES. AT DAY 10.5, EXPRESSED IN THE MYOTOME COMPARTMENT OF SOMITES. AT LATER STAGES OF DEVELOPMENT, DETECTED IN A WIDE RANGE OF DEVELOPING MUSCLES. EXPRESSION CONTINUES IN ADULTHOOD.

CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC

EMBL; U84005; AAC53167; 1; -

DR HSSP; P18075; 1BMP.

DR MGDB; MGI:95631; Gdf8.

DR InterPro; IPK001839; TGF-beta.

DR SMART; SM00204; TGFb\_N.

DR Pfam; PF00019; TGF-beta; 1.

DR Pfam; PF00688; TGFb\_propeptide; 1.

DR PRODOM; PDD00357; TGF-beta; 1.  
 DR SMART; SM0204; TGF-BETA; 1.  
 KW PROSIRE; P502250; TGF-BETA; 1.  
 KW GROWTH factor; Cytokine; Glycoprotein; Signal.  
 FT SIGNAL 1 24 POTENTIAL.  
 FT PROPEP 25 267 GROWTH/DIFFERENTIATION FACTOR 8.  
 FT CHAIN 268 376 FT CHAIN 268 376 GROWTH/DIFFERENTIATION FACTOR 8.  
 FT DISULFID 282 341 FT DISULFID 282 341 BY SIMILARITY.  
 FT DISULFID 310 373 FT DISULFID 310 373 BY SIMILARITY.  
 FT DISULFID 314 375 FT DISULFID 314 375 BY SIMILARITY.  
 FT DISULFID 340 370 FT DISULFID 340 370 INTERCHAIN (BY SIMILARITY).  
 FT CARBONID 72 72 FT CARBONID 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 376 AA; 42921 MW; 933043DGC8C3394B CRC64;

Query Match 99.0%; score 622; DB 1; Length 376;  
 Best Local Similarity 99.1%; pred. No. 4e-63; 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 108; Conservative 0; P: Mismatches 1; I: Indels 0; G: Gaps 0;

Qy 1 DFGLQDEHESRSRCRYPITVDFEARFGWMILAKRKYKANYCSCGCEVFLOQKPHTL 60  
 Db 268 DFGLQDEHESRSRCRYPITVDFEARFGWMILAKRKYKANYCSCGCEVFLOQKPHTL 327  
 61 VHQANPRGSAAGPCCTPTLMSPINMLYFNGKBOIYGKIPANVDRGCGS 109  
 328 VHQANPRGSAAGPCCTPTKMSPINMLYFNGKBOIYGKIPANVDRGCGS 376

RESULT 6  
 GDF8\_RAT STANDARD; PRT; 376 AA.  
 AC 035312; 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).  
 GN GDF8 OR MSTN.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N A.  
 RC TISSUE-Skeletal muscle;  
 RC MEDLINE=98024153; PubMed=9356471;  
 RA McPherron A.C., Lee S.-J.;  
 RT "Double muscling in cattle due to mutations in the myostatin gene.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).  
 CC -I- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL  
 CC TISSUE-Skeletal muscle;  
 CC MEDLINE=98024153; PubMed=9356471;  
 CC McPherron A.C., Lee S.-J.;  
 CC "Double muscling in cattle due to mutations in the myostatin gene.";  
 CC Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).  
 CC -I- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL  
 CC MUSCLE GROWTH.  
 CC -I- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).  
 CC -I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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 or send an email to license@isb-sib.ch).

CC EMBL; AF019624; AAB86691.1. -.  
 DR PRODOM; PDD00357; TGF-beta; 1.  
 DR SMART; SM0204; TGF-BETA; 1.  
 DR InterPro; IPR01111; TGFb\_N.  
 DR Pfam; PF00019; TGF-beta; 1.  
 DR Pfam; PF00688; TGFb\_Propeptide; 1.  
 DR PRODOM; PDD00357; TGF-beta; 1.  
 DR SMART; SM0204; TGF-BETA; 1.  
 DR InterPro; IPR01111; TGFb\_N.  
 DR Pfam; PF00019; TGF-beta; 1.  
 DR PRODOM; PDD00357; TGF-beta; 1.  
 DR SMART; SM0204; TGF-BETA; 1.  
 DR InterPro; IPR01111; TGFb\_N.  
 DR Pfam; PF00688; TGFb\_Propeptide; 1.  
 DR PRODOM; PDD00357; TGF-beta; 1.  
 DR SMART; SM0204; TGF-BETA; 1.  
 DR InterPro; IPR01111; TGFb\_N.  
 DR Pfam; PF00019; TGF-beta; 1.  
 DR PROPEP 25 267 FT PROPEP 24 266 GROWTH/DIFFERENTIATION FACTOR 8.  
 FT CHAIN 267 375 FT CHAIN 267 375 BY SIMILARITY.  
 FT DISULFID 281 340 FT DISULFID 281 340 BY SIMILARITY.  
 FT DISULFID 309 372 FT DISULFID 309 372 BY SIMILARITY.  
 FT DISULFID 339 339 FT DISULFID 339 339 INTERCHAIN (BY SIMILARITY).



DR Pfam: PR00019; TGF-beta; 1.  
 DR Pfam: PR00588; TGFb\_propeptide; 1.  
 DR Problem: PR000357; TGF-beta; 1.  
 DR SMART: SM00204; TGFb; 1.  
 DR PROSITE: PS00250; TGF\_BETA\_1; 1.  
 DR Growth factor; Cytokine; Glycoprotein; signal; disease mutation.  
 KW SIGNAL 1 18 POTENTIAL.  
 FT PROPEP 19 266 POTENTIAL.  
 FT CHAIN 267 375 GROWTH/DIFFERENTIATION FACTOR 8.  
 FT DISULFID 281 340 BY SIMILARITY.  
 FT DISULFID 309 372 BY SIMILARITY.  
 FT DISULFID 313 374 BY SIMILARITY.  
 FT DISULFID 339 339 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARIANT 94 94 F -> L (IN MH; PIEDMONTSE BREED).  
 FT VARIANT 313 313 C -> Y (IN MH; PIEDMONTSE BREED).  
 FT CONFLICT 14 14 T -> M (IN REF. 2).  
 SQ SEQUENCE 375 AA; 42520 MW; E1B791AB9D4A9E6 CRC64;

Query Match 97.3%; Score 611; DB 1; Length 375;  
 Best Local Similarity 97.2%; Pred. No. 7.1e-62;  
 Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DFGLCDCDEHSTESRCRCRYPTVDFEAGFMWILAKPKRYKANYCSECEFVFLQKYPTHL 60  
 Db 267 DFGLCDCDEHSTESRCRCRYPTVDFEAGFMWILAKPKRYKANYCSECEFVFLQKYPTHL 326

Qy 61 VHQANPRGSGPCCPTPLMSPINMLYFNGKEQITYKGKIPAMVDRGCS 109  
 Db 327 VHQANPRGSGPCCPTKMSPINMLYFNGKEQITYKGKIPAMVDRGCS 375

RESULT 10  
 GDFB\_MOUSE  
 ID GDFB\_MOUSE STANDARD; PRT; 405 AA.  
 AC Q9ZLW4; Q9YX55; Q9RZ21;  
 DT 16-OCT-2001 (Rel. 40; Created)  
 DT 16-OCT-2001 (Rel. 40; Last sequence update)  
 DT 16-OCT-2001 (Rel. 40; Last annotation update)  
 DE Growth/differentiation factor 11 precursor (Bone morphogenetic protein 11).  
 DE GDF11 OR BMP11.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TAXID=10990;  
 RN [1] SEQUENCE FROM N.A.  
 RX MEDLINE=9917755; PubMed=10075854;  
 RA Gamer L.W., Wolfman N.M., Celeste A.J., Hattersley G., Hewick R.,  
 RA Rosen V.  
 RT "A novel BMP expressed in developing mouse limb, spinal cord, and tail  
 bud is a potent mesoderm inducer in Xenopus embryos.",  
 RL Dev. Biol. 208:222-232(1999).  
 RN [2] SEQUENCE FROM N.A.  
 RP STRAIN=129/SVJ;  
 RX MEDLINE=99318097; PubMed=10391213;  
 RA McPherson A.C., Lawler A.M., Lee S.-J.;  
 RA "Regulation of anterior/posterior patterning of the axial skeleton by growth/differentiation factor 11.",  
 RL Nat. Genet. 22:260-264 (1999).  
 RN [3] SEQUENCE OF 75-405 FROM N.A.  
 RX MEDLINE=99177567; PubMed=10072786;  
 RA Nakashima M., Toyono T., Akamine A., Joyner A.;  
 RT "Expression of growth/differentiation factor 11, a new member of the BMP/TGFbeta superfamily during mouse embryogenesis.",  
 RL Mech. Dev. 80:185-189 (1999).  
 CC -1- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL  
 CC -1- IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.

CC PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN.  
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).  
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE DEVELOPING LIMB BUD, INITIALLY DETECTED IN THE DISTAL MESENCHIME, AND LATER LOCALIZING TO REGIONS AROUND THE DEVELOPING BONES, IS ALSO EXPRESSED IN ADULT DENTAL PULP AND BRAIN.  
 CC -1- DEVELOPMENTAL STAGE: FIRST STRONGLY EXPRESSED IN RESTRICTED DOMAINS AT 8-5 DAYS POST COITUS (DPC) WHERE IT IS HIGHEST IN THE TRAIL BUD. AT 10.5 DPC, EXPRESSED IN THE BRANCHIAL ARCHES, LIMB BUD, TAIL BUD AND POSTERIOR DORSAL NEURAL TUBE. LATER, EXPRESSED IN TERMINALLY-DIFFERENTIATED ODDONTOBLASTS, THE NASAL EPITHELIUM, RETINA AND SPECIFIC REGIONS OF THE BRAIN.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the European Bioinformatics Institute and the EMBL outstation - use by non-profit institutions as long as no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).  
 CC -----  
 DR EMBL; AF092734; AAD05267.1; -.  
 DR EMBL; AF092734; AAD05267.1; -.  
 DR EMBL; AF100904; AAC72853.1; JOINED.  
 DR EMBL; AF100905; AAC72853.1; JOINED.  
 DR EMBL; AF028337; AACF21633.1; -.  
 DR EMBL; AF028335; AACF21633.1; JOINED.  
 DR EMBL; AF028336; AACF21633.1; JOINED.  
 DR EMBL; P18075; IBMP.  
 DR HSSP; P18075; IBMP.  
 DR MGI; J338027; Gdf11.  
 DR InterPro; IPR001839; TGF-beta.  
 DR InterPro; IPR001111; TGF-beta.  
 DR Pfam; PR00011; TGF-beta.1.  
 DR Pfam; PR00588; TGFb\_propeptide; 1.  
 DR SMART; SM00204; TGFb; 1.  
 DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 KW SIGNAL 1 20 POTENTIAL.  
 FT PROPEP 21 296 BY SIMILARITY.  
 FT CHAIN 297 405 GROWTH/DIFFERENTIATION FACTOR 11.  
 FT DOMAIN 29 39 POLY-ALA.  
 FT DOMAIN 208 213 POLY-GLY.  
 FT DISULFID 311 370 BY SIMILARITY.  
 FT DISULFID 339 402 BY SIMILARITY.  
 FT DISULFID 343 404 BY SIMILARITY.  
 FT DISULFID 369 369 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 75 75 E -> G (IN REF. 3).  
 FT CONFLICT 171 171 T -> M (IN REF. 2).  
 SQ SEQUENCE 405 AA; 44946 MW; A7413822/10A14781 CRC64;

Query Match 91.4%; Score 574; DB 1; Length 405;  
 Best Local Similarity 89.0%; Pred. No. 1.2e-57; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DFGLCDCDEHSTESRCRCRYPTVDFEAGFMWILAKPKRYKANYCSECEFVFLQKYPTHL 60  
 Db 297 NLGLDCDCDEHSTESRCRCRYPTVDFEAGFMWILAKPKRYKANYCSECEFVFLQKYPTHL 356

Qy 61 VHQANPRGSGPCCPTPLMSPINMLYFNGKEQITYKGKIPAMVDRGCS 109  
 Db 357 VHQANPRGSGPCCPTKMSPINMLYFNGKEQITYKGKIPAMVDRGCS 405

RESULT 11  
 GDFB\_HUMAN  
 ID GDFB\_HUMAN STANDARD;  
 AC Q95390; Q9UD1; Q9UD2;  
 CC PRT; 407 AA.

Query Match 91.4%; Score 574; DB 1; Length 407;  
 Best Local Similarity 89.0%; Pred. No. 1.2e-57;  
 Matches 97; Conservative 7; Mismatches 5; Indels 0; Gaps 0  
 Qy 1 DFGLCDCEHISTEGRCCRCPVPLTVDFEAFGDWIATPKRYKANYSGCECEVFVLOKYPHTHL 60



Query Match Similarity 38.4%; Score 241; DB 1; Length 255; Best Local Similarity 42.4%; Pred. No. 4e-20; Matches 50; Conservative 17; Mismatches 37; Indels 14; Gaps 6; DB 255 AA: 29178 MW; 2524B21DC648D9A9 CRC64; Sequence

DR pfam: PF00688; TGFb\_propeptide; 1.  
DR PRINTS: PR00438; GRCYSKN0.  
DR PRODOM: PD00057; TGF-*beta*; 1.  
DR SMART: SM0204; TGF-*beta*; 1.  
DR PROSITE: PS00250; TGF-*BETA\_1*; 1.  
DR KW growth factor; Mitogen; Glycoprotein; Signal.  
FT SIGNAL 1 15 POTENTIAL.  
FT PROPEP 16 240 DVR-1 PROTEIN.  
FT CHAIN 241 355 BY SIMILARITY.  
FT DISULFID 254 320 BY SIMILARITY.  
FT DISULFID 283 352 BY SIMILARITY.  
FT DISULFID 319 319 INTERCHAIN (BY SIMILARITY).  
FT CARBOHYD 108 108 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT SEQUENCE 355 AA: 40201 MW; 0ED5B9850EBFB222 CRC64;

Query Match Similarity 38.4%; Score 241; DB 1; Length 255; Best Local Similarity 42.4%; Pred. No. 4e-20; Matches 50; Conservative 17; Mismatches 37; Indels 14; Gaps 6; DB 198 AA: 29178 MW; 2524B21DC648D9A9 CRC64; Sequence

DR pfam: PF00688; TGFb\_propeptide; 1.  
DR PRINTS: PR00438; GRCYSKN0.  
DR PRODOM: PD00057; TGF-*beta*; 1.  
DR SMART: SM0204; TGF-*beta*; 1.  
DR PROSITE: PS00250; TGF-*BETA\_1*; 1.  
DR KW growth factor; Mitogen; Glycoprotein; Signal.  
FT SIGNAL 1 15 POTENTIAL.  
FT PROPEP 16 240 DVR-1 PROTEIN.  
FT CHAIN 241 355 BY SIMILARITY.  
FT DISULFID 254 320 BY SIMILARITY.  
FT DISULFID 283 352 BY SIMILARITY.  
FT DISULFID 319 319 INTERCHAIN (BY SIMILARITY).  
FT CARBOHYD 108 108 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT SEQUENCE 355 AA: 40201 MW; 0ED5B9850EBFB222 CRC64;

Query Match Similarity 38.1%; Score 239; DB 1; Length 355; Best Local Similarity 43.4%; Pred. No. 9.5e-20; Matches 46; Conservative 16; Mismatches 36; Indels 8; Gaps 3; DB 255 AA: 40201 MW; 0ED5B9850EBFB222 CRC64; Sequence

DR pfam: PF00688; TGFb\_propeptide; 1.  
DR PRINTS: PR00438; GRCYSKN0.  
DR PRODOM: PD00057; TGF-*beta*; 1.  
DR SMART: SM0204; TGF-*beta*; 1.  
DR PROSITE: PS00250; TGF-*BETA\_1*; 1.  
DR KW growth factor; Mitogen; Glycoprotein; Signal.  
FT SIGNAL 1 15 POTENTIAL.  
FT PROPEP 16 240 DVR-1 PROTEIN.  
FT CHAIN 241 355 BY SIMILARITY.  
FT DISULFID 254 320 BY SIMILARITY.  
FT DISULFID 283 352 BY SIMILARITY.  
FT DISULFID 319 319 INTERCHAIN (BY SIMILARITY).  
FT CARBOHYD 108 108 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT SEQUENCE 355 AA: 40201 MW; 0ED5B9850EBFB222 CRC64;

Search completed: May 20, 2002, 09:24:50  
Job time: 215 sec

RESULT 15

DVR1_BRARE	STANDARD;	PRT:	355 AA.
AC P35621;			
DT 01-JUN-1994 (Rel. 29, created)			
DT 01-JUN-1994 (Rel. 29, last sequence update)			
DT 01-MAR-2002 (Rel. 41, last annotation update)			
DE DVR-1 protein precursor.			
GN VGI OR DVR1 OR DVR-1.			
OS Brachydanio rerio (Zebrafish)			
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.			
OX NCBI_TaxID=7955;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Embryo;			
RX MEDLINE=9400920; PubMed=8405668;			
RA Heide K.A., Grunwald D.J.;			
RT "The DVR-1 (vgl) transcript of zebrafish is maternally supplied and distributed throughout the embryo.";			
RL Dev. Biol. 159:418-426(1993).			
CC -!- FUNCTION: SERVES TO FACILITATE THE DIFFERENTIATION OF EITHER MESODERM OR ENDODERM EITHER AS A COFACTOR IN AN INSTRUCTIVE SIGNAL OR BY PROVIDING PERMISSIVE ENVIRONMENT.			
CC -!- SUBUNIT: HOMODIMER (PROBABLE).			
CC -!- TISSUE SPECIFICITY: ABUNDANT IN OVARIES AND EGGS, AND EQUALLY DISTRIBUTED AMONG ALL BLASTOMERES.			
CC -!- DEVELOPMENTAL STAGE: CONCENTRATED IN THE STREAMING CYTOPLASM IN JUST-FERTILIZED EGGS. EVENLY PARTITIONED DURING CLEAVAGE AMONG ALL BLASTOMERES. ABSENT IN THE Yolk CELL DURING CLEAVAGE, BLASTULA AND GASTRULA STAGES. DISTRIBUTED HOMOGENEOUSLY AMONG ALL CELLS OF THE GASTRULA.			
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.			

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EMBL: 000931; AAC27347.1; -.

HSSP: PI2643; 3BMP.

ZFIN: ZDB-GENE-980526-309; dvr1.

DR InterPro: IPR002400; GF-cystkn.

DR InterPro: IPR001839; TGF-beta.

DR InterPro: IPR001111; IGB\_N.

DR Ptam: PF00019; TGF-beta; 1.





QY	1	DFGLDCDEHSTESRCRCRYPTLVDFAFGWMWIAPKRKYANCGCCECFVFLQYPHTL 60	RA	Smock, S. L.; Owen, T. A.;
Db	54	DFGLDCDEHSTESRCRCRYPTLVDFAFGWMWIAPKRKYANCGCCECFVFLQYPHTL 113	RT	"Cloning of the open reading frame DNA for macaque fascicularis
Qy	61	VHQANPRGSAGCCPTLMSPINMLYFNGEQIYKGKIPAMVDRGCS 109	RT	( <i>Cynomolgus macaque</i> ) myostatin (Gp188).";
Db	114	VHQANPRGSAGCCPTKMSPINMLYFNGEQIYKGKIPAMVDRGCS 162	RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RESULT	2		DR	EMBL; AY055750; RALI7640_1; -.
ID	Q9GM97	PRELIMINARY;	PRT;	375 AA.
AC	Q9GM97;			
DT	01-MAR-2001 (TREMBrel. 16, created)			
DT	01-MAR-2001 (TREMBrel. 16, last sequence update)			
DT	01-DIC-2001 (TREMBrel. 19, last annotation update)			
DE	MYOSTATIN.			
GN	MSN.			
OS	Equus caballus (Horse).			
OC	Eukaryote; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.			
OX	NCBI_TaxID=9796;			
[1]	SEQUENCE FROM N-A.			
RC	STRAIN=THROUGHBRED;			
RA	Hosoyama T., Yamamoto K., Tojo H., Tachi C.;			
RT	"Molecular cloning of equine myostatin cDNA and serum level of myostatin in horse.";			
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.			
CC	-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.			
EMBL	AB033541; BAB16046_1; -.			
DR	HSSP; P18075; 1BMP			
DR	InterPro; IPR002048; EF-hand			
DR	InterPro; IPR001839; TGF-beta.			
DR	InterPro; IPR001111; TGFBN.			
DR	Pfam; PF00019; TGF-beta; 1.			
DR	ProDom; PD000357; TGF-beta; 1.			
DR	SMART; SM00204; TGFBN.			
DR	PROSITE; PS00018; EF_HAND; UNKNOWN_1.			
SQ	SEQUENCE 375 AA; 42736 MW; 6F424ECBEB4D9936 CRC64;			
RESULT	4			
ID	Q98SP0	PRELIMINARY;	PRT;	375 AA.
AC	Q98SP0;			
DT	01-JUN-2001 (TREMBrel. 17, created)			
DT	01-JUN-2001 (TREMBrel. 17, last sequence update)			
DT	01-DEC-2001 (TREMBrel. 19, last annotation update)			
DE	MYOSTATIN.			
GN	MSN.			
OS	Gallus gallus (Chicken).			
OC	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.			
OX	NCBI_TaxID=9031;			
RN	SEQUENCE FROM N-A.			
RP	Zhang Y., Yang W., Zhu D.;			
RT	"Genomic structure and expression of the chicken GDF-8 during development.";			
RT	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.			
CC	-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.			
DR	EMBL; AF368599; AAK18001_1; -.			
DR	HSSP; P18075; 1BMP.			
DR	InterPro; IPR002048; EF-hand.			
DR	InterPro; IPR001839; TGF-beta.			
DR	InterPro; IPR001111; TGFBN.			
DR	Pfam; PF00019; TGF-beta; 1.			
DR	ProDom; PD000357; TGF-beta; 1.			
DR	SMART; SM00204; TGFBN.			
DR	PROSITE; PS00018; EF_HAND; UNKNOWN_1.			
KW	Glycoprotein.			
SQ	SEQUENCE 375 AA; 42717 MW; D980E286426E4D4F CRC64;			
RESULT	3			
Q95J86	SEQUENCE FROM N-A.			
ID	095J86	PRELIMINARY;	PRT;	375 AA.
AC	095J86;			
DR	01-DEC-2001 (TREMBrel. 19, created)			
DT	01-DEC-2001 (TREMBrel. 19, last sequence update)			
DT	01-DEC-2001 (TREMBrel. 19, last annotation update)			
DE	MYOSTATIN.			
OS	Macaca fascicularis (Crab eating macaque) ( <i>Cynomolgus monkey</i> ).			
OC	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.			
OC	NCBI_TaxID=9541;			
OX	{1}			
RP	SEQUENCE FROM N-A.			
RC	TISSUE-GASTROCNEMIUS;			
RESULT	5			
ID	Q95N97	PRELIMINARY;	PRT;	375 AA.
AC	Q95N97;			
DT	01-DEC-2001 (TREMBrel. 19, last sequence update)			
DT	01-DEC-2001 (TREMBrel. 19, last annotation update)			
DE	MYOSTATIN.			
OS	Macaca fascicularis (Crab eating macaque) ( <i>Cynomolgus monkey</i> ).			
OC	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.			
OC	NCBI_TaxID=9541;			
OX	{1}			
RP	SEQUENCE FROM N-A.			
RC	TISSUE-GASTROCNEMIUS;			

AC	Q95N97;	Score 95.4%;	DB 6;	Length 185;	RESULT 7
DT	01-DEC-2001 (TREMBrel. 19, Last sequence update)				Q9M218
DT	01-DEC-2001 (TREMBrel. 19, Last annotation update)				Q9M218 PRELIMINARY; PRM; 185 AA.
DE	MYOSTATIN.				AC Q9M218;
GN	GDF8;				DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)
OS	Bos taurus (Bovine).				DT 01-OCT-2000 (TREMBrel. 19, Last annotation update)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.				DE MYOSTATIN (FRAGMENT).
OC	NCBI_TaxID=9913;				OS OVIS aries (Sheep).
RN	[1]				OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Ovis.
RP	SEQUENCE FROM N.A.				OC
RX	MEDLINE=21343337; PubMed=11451380;				OX NCBI_TaxID=9940;
RA	Jeanplong F., Sharma M., Somers W.G., Bass J.J., Kambadur R.;				RN [1]
RT	"Genomic organization and neonatal expression of the bovine myostatin gene.";				RP SEQUENCE FROM N.A.
PT	Mol. cell. Biochem. 220:31-37 (2001).				RA Lian Z., Jin H., Li N.;
EMBL	AF320998; ARG48116.1; -;				RT "Cloning of intron 2 of the myostatin gene in sheep."
SRQ	SEQUENCE 375 AA; 42551 MW; 84E1AB20650C05F6 CRC64;				RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
Best Local Similarity 97.3%; Score 611; DB 6; Length 375; Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;					CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
QY 1 DFGLCDDEHSTESRCRCRYPLTVDFEAFCGDWIAIPKRYKANYCNSGCGCEVFVFLQKYPTHL 60					DR EMBL; AF266758; AAF78069.1; -;
Db 267 DFGLCDDEHSTESRCRCRYPLTVDFEAFCGDWIAIPKRYKANYCNSGCGCEVFVFLQKYPTHL 326					DR HSSP; P12643; 3BMP.
DE MYOSTATIN (FRAGMENT).					DR Interpreter; IPK001339; TGF-beta.
GN MSTN.					DR Pfam; PF00019; TGF-beta; 1.
OS Capra hircus (Goat).					DR P000357; TGF-beta; 1.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; capra.					DR SMART; SM00204; TGF-B; 1.
OC NCBI_TaxID=9925;					DR PROSITE; PS00250; TGF_BETA; 1.
RN [1]					FT KW Glycoprotein.
RP SEQUENCE FROM N.A.					FT NON-TER 1 1
RA Lian Z., Pan Q., Chen H., Jin H., Li N.;					FT NON-TER 185 185
RT "Cloning of intron 2 of the myostatin gene in goat.";					FT SEQUENCE 185 AA; 20923 MW; BA9634203A552850 CRC64;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.					QY 1 DFGLCDDEHSTESRCRCRYPLTVDFEAFCGDWIAIPKRYKANYCNSGCGCEVFVFLQKYPTHL 60
DR EMBL; AY032689; AAK49790.1; -;					Db 79 DFGLCDDEHSTESRCRCRYPLTVDFEAFCGDWIAIPKRYKANYCNSGCGCEVFVFLQKYPTHL 138
FT NON-TER 1 1					QY 61 VHOANPRGSAGCCTPTLSPINMLYFNGKEQIYGKIPAMVYDRCG 107
SEQUENCE 185 AA; 20953 MW; 03675B38E9D64D4 CRC64;					Db 139 VHOANPRGSAGCCTPTKMSPINMLYFNGKEQIYGKIPAMVYDRCG 185
RESULT 6					Query Match 94.3%; Score 592; DB 6; Length 185; Best Local Similarity 95.3%; Pred. No. 1.9e-63; Matches 102; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Q95N11					Query Match 95.4%; Score 599; DB 6; Length 185; Best Local Similarity 96.3%; Pred. No. 2.8e-64; Matches 103; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
PRELIMINARY; PRT; 185 AA.					RESULT 8
Q95N11					Q9OYY0 PRELIMINARY; PRM; 389 AA.
AC Q95N11; 01-DEC-2001 (TREMBrel. 19, Last sequence update)					ID Q9OYY0
DR 01-DEC-2001 (TREMBrel. 19, Last annotation update)					AC Q9OYY0;
DE MYOSTATIN.					DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)
GN Ictalurus punctatus (Channel catfish).					DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Osteichthyes; Actinopterygii; Teleostei; Ostariophysi; Siluriformes; Ictaluridae; Ictalurus.					OS Ictalurus punctatus (Channel catfish).
OC	NCBI_TaxID=998;				OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Osteichthyes; Actinopterygii; Teleostei; Ostariophysi; Siluriformes; Ictaluridae; Ictalurus.
RN [1]					OC
RP SEQUENCE FROM N.A.					NCBI_TaxID=998;
RA Kocabas A.M., Liu Z.J.;					RN [1]
RT "Molecular characterization and expression of the myostatin gene from channel catfish (Ictalurus punctatus).";					RP SEQUENCE FROM N.A.
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.					RA Kocabas A.M., Liu Z.J.;
DR EMBL; AF39647; AAK84566.1; -;					RT "Molecular characterization and expression of the myostatin gene from channel catfish (Ictalurus punctatus).";
SQ SEQUENCE 389 AA; 43600 MW; 569FB952B7E9E173 CRC64;					RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
Query Match 89.6%; Score 563; DB 13; Length 389; Best Local Similarity 89.7%; Pred. No. 1.3e-59; Matches 96; Conservative 8; Mismatches 3; Indels 0; Gaps 0;					DR EMBL; AF39647; AAK84566.1; -;
QY 61 VHOANPRGSAGCCTPTLSPINMLYFNGKEQIYGKIPAMVYDRCG 107					SQ SEQUENCE 389 AA; 43600 MW; 569FB952B7E9E173 CRC64;
Db 139 VHOANPRGSAGCCTPTKMSPINMLYFNGKEQIYGKIPAMVYDRCG 185					

QY	3	GLIDCDEHISTESRCRCPYPLVDFEAFGWNWIAPIKRYKANYCSCBCEFVFLQKYPHTHLR	RP
Db	283	GLIDCDEHISTESRCRCPYPLVDFEAFGWNWIAPIKRYKANYCSCBCEFVFLQKYPHTHLR	RA
QY	63	QANPRGSGAGCPCTPLMSPINMLYFNGKEQIYKIPAMVDRGCS 109	RA
Db	343	KANPRGTAGPCCTPKMSPINMLYFNGKEQIYKIPAMVDRGCS 389	RT
RESULT	9		"The two myostatin genes of Atlantic salmon ( <i>Salmo salar</i> ) are expressed in a variety of tissues.";
ID	Q90W05	PRELIMINARY;	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
AC	Q90W05;	PRT;	-1 SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DE	MYOSTATIN		
OS	Sparus aurata (Gilthead sea bream).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; perciformes; Percidae; Sparidae; Sparus.		
OC	MacCioni L., Bargelloni L., Radella G., Mascarello F., Patarrelio T.,		
RA	"Characterization of the myostatin gene in the gilthead seabream, <i>Sparus aurata</i> : sequence, genomic structure, and expression pattern.";		
RT	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF258448; AAK53454.1; -		
DR	EMBL; AF258447; AAK53454.1; -		
DR	SEQUENCE 385 AA; 43704 MW; 18F902CE325A3916 CRC64;		
Query Match	89.2%	Score 560; DB 13; Length 385;	
Best Local Similarity	89.0%	Pred. No. 3e-59; Mismatches 6; Indels 0; Gaps 0;	
Matches	97;	Conservative 6; Mismatches 6; Indels 0; Gaps 0;	
QY	1	DGLDCDEHISTESRCRCPYPLVDFEAFGWNWIAPIKRYKANYCSCBCEFVFLQKYPHTHL 60	QY
RT	"Two myostatin genes are differentially expressed in myotomal muscle of the trout ( <i>Oncorhynchus mykiss</i> ).";		
Db	277	DGLDCDEHISTESRCRCPYPLVDFEAFGWNWIAPIKRYKANYCSCBCEFVFLQKYPHTHL 336	Db
QY	61	VHQANPRGSGAGCPCTPLMSPINMLYFNGKEQIYKIPAMVDRGCS 109	QY
DR	EMBL; AF273035; AAKY1707.1; -		
DR	SEQUENCE 337 AA; 42049 MW; 9DD4771B5CF671EA CRC64;		
RESULT	10		
ID	Q90ZD1	PRELIMINARY;	
AC	Q90ZD2	PRT;	
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DE	MYOSTATIN 1.		
OS	<i>Oncorhynchus mykiss</i> (Rainbow trout) ( <i>Salmo gairdneri</i> ).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Buteleostomi; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.		
RA	MacCioni L., Bargelloni L., Radella G., Mascarello F., Patarrelio T.,		
RA	"Characterization of the myostatin gene in the gilthead seabream, <i>Sparus aurata</i> : sequence, genomic structure, and expression pattern.";		
RT	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF258448; AAK53454.1; -		
DR	EMBL; AF258447; AAK53454.1; -		
DR	SEQUENCE 385 AA; 43704 MW; 18F902CE325A3916 CRC64;		
Query Match	88.7%	Score 557; DB 13; Length 373;	
Best Local Similarity	88.1%	Pred. No. 6.7e-59; Mismatches 7; Indels 0; Gaps 0;	
Matches	96;	Conservative 7; Mismatches 7; Indels 0; Gaps 0;	
QY	1	DGLDCDEHISTESRCRCPYPLVDFEAFGWNWIAPIKRYKANYCSCBCEFVFLQKYPHTHL 60	QY
RT	"Two myostatin genes are differentially expressed in myotomal muscle of the trout ( <i>Oncorhynchus mykiss</i> ).";		
Db	265	DGLDCDEHISTESRCRCPYPLVDFEAFGWNWIAPIKRYKANYCSCBCEFVFLQKYPHTHL 324	Db
QY	61	VHQANPRGSGAGCPCTPLMSPINMLYFNGKEQIYKIPAMVDRGCS 109	QY
DR	EMBL; AF273035; AAKY1707.1; -		
DR	SEQUENCE 373 AA; 42049 MW; 9DD4771B5CF671EA CRC64;		
RESULT	11		
ID	Q90ZD2	PRELIMINARY;	
AC	Q90ZD2	PRT;	
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DE	MYOSTATIN 1.		
OS	<i>Oncorhynchus mykiss</i> (Rainbow trout) ( <i>Salmo gairdneri</i> ).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Buteleostomi; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.		
RA	MacCioni L., Bargelloni L., Radella G., Mascarello F., Patarrelio T.,		
RA	"Characterization of the myostatin gene in the gilthead seabream, <i>Sparus aurata</i> : sequence, genomic structure, and expression pattern.";		
RT	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF258448; AAK53454.1; -		
DR	EMBL; AF258447; AAK53454.1; -		
DR	SEQUENCE 373 AA; 42049 MW; 9DD4771B5CF671EA CRC64;		
Query Match	88.7%	Score 557; DB 13; Length 373;	
Best Local Similarity	88.1%	Pred. No. 6.7e-59; Mismatches 7; Indels 0; Gaps 0;	
Matches	96;	Conservative 7; Mismatches 6; Indels 0; Gaps 0;	
QY	1	DGLDCDEHISTESRCRCPYPLVDFEAFGWNWIAPIKRYKANYCSCBCEFVFLQKYPHTHL 60	QY
RT	"Two myostatin genes are differentially expressed in myotomal muscle of the trout ( <i>Oncorhynchus mykiss</i> ).";		
Db	265	DGLDCDEHISTESRCRCPYPLVDFEAFGWNWIAPIKRYKANYCSCBCEFVFLQKYPHTHL 324	Db
QY	61	VHQANPRGSGAGCPCTPLMSPINMLYFNGKEQIYKIPAMVDRGCS 109	QY
DR	EMBL; AF273035; AAKY1707.1; -		
DR	SEQUENCE 373 AA; 42049 MW; 9DD4771B5CF671EA CRC64;		
RESULT	12		
ID	Q90ZD1	PRELIMINARY;	
AC	Q90ZD1	PRT;	
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DE	MYOSTATIN 1.		
OS	<i>Salmo salar</i> (Atlantic salmon). Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.		
OC	MacCioni L., Bargelloni L., Radella G., Mascarello F., Patarrelio T.,		
OC	"The two myostatin genes of Atlantic salmon ( <i>Salmo salar</i> ) are expressed in a variety of tissues.";		
RT	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF273035; AAKY1707.1; -		
DR	SEQUENCE FROM N.A.		
RA	Ostbye T.K., Galloway T.F., Nielsen C., Gabestad I., Bardal T.;		
RA	"The two myostatin genes of Atlantic salmon ( <i>Salmo salar</i> ) are expressed in a variety of tissues.";		
RT	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AJ292267; CAC9541.2; -		
DR	EMBL; AJ316006; CAC9700.1; -		
DR	HSSP; P12643; 3BMP		
DR	InterPro; IPR001839; TGF beta.		
DR	SMART; SM00204; TGFb; 1.		
DR	PROSITE; PS000220; TGF-BETA; 1.		
KW	glycoprotein; Signal		
FT	SIGNAL 1 22 POTENTIAL.		
FT	CHAIN 265 373 MYOSTATIN.		
SQ	SEQUENCE 373 AA; 41896 MW; C641D71D33E66C4D CRC64;		
Query Match	88.7%	Score 557; DB 13; Length 373;	
Best Local Similarity	88.1%	Pred. No. 6.7e-59; Mismatches 7; Indels 0; Gaps 0;	
Matches	96;	Conservative 7; Mismatches 7; Indels 0; Gaps 0;	
QY	1	DGLDCDEHISTESRCRCPYPLVDFEAFGWNWIAPIKRYKANYCSCBCEFVFLQKYPHTHL 60	QY
RT	"Two myostatin genes are differentially expressed in myotomal muscle of the trout ( <i>Oncorhynchus mykiss</i> ).";		
Db	265	DGLDCDEHISTESRCRCPYPLVDFEAFGWNWIAPIKRYKANYCSCBCEFVFLQKYPHTHL 324	Db
QY	61	VHQANPRGSGAGCPCTPLMSPINMLYFNGKEQIYKIPAMVDRGCS 109	QY
DR	EMBL; AF273035; AAKY1707.1; -		
DR	SEQUENCE 373 AA; 42049 MW; 9DD4771B5CF671EA CRC64;		
RESULT	13		
ID	Q90ZD1	PRELIMINARY;	
AC	Q90ZD1	PRT;	
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DE	MYOSTATIN 1.		
OS	<i>Salmo salar</i> (Atlantic salmon). Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.		
OC	MacCioni L., Bargelloni L., Radella G., Mascarello F., Patarrelio T.,		
OC	"The two myostatin genes of Atlantic salmon ( <i>Salmo salar</i> ) are expressed in a variety of tissues.";		
RT	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF273035; AAKY1707.1; -		
DR	SEQUENCE FROM N.A.		
RA	Anderesen O.;		
RA	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.		
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.		
RN			

AC	090201;	DT	01-DEC-2001 (TREMBLrel. 19, Created)
RP	RA	RT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
RN	SEQUENCE FROM N.A.	RT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
RP	Rescan P.-Y., Jutel I., Ralliere C.;	RT	MYOSTATIN 2.
RN	"Two myostatin genes are differentially expressed in myotomal muscle of the trout ( <i>Oncopterus mykiss</i> ).";	RL	<i>Oncopterus mykiss</i> (Rainbow trout) ( <i>Salmo gairdneri</i> ).
RP	J. EXP. BIOL. 0:0-0 (2001);	DR	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Euteleostomi; Protacanthopterygii; Salmoniformes; Salmonidae; <i>Oncorhynchus</i> . NCBI_TAXID=8022;
QY	1 DFGLCDDEHTESRCRCRYPTLVDFAFGWMWIAPIRKYKANYCSCGCEFFVFLQKYPHTHL 60	Db	328 VNKANPRTAGPCCPTKMSPINMLYFNRKQIYGKIPSMVWDRCGCS 376
Q90WC9	PRELIMINARY;	Q90WC9;	Q90WC9;
Q90WC9;	PRT; 376 AA.	Q90WC9;	Q90WC9;
Q90WC9;	RT	01-DEC-2001 (TREMBLrel. 19, Created)	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
Q90WC9;	DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
Q90WC9;	DR	MYOSTATIN;	MYOSTATIN;
Q90WC9;	OS	Morone saxatilis (Striped bass).	Morone saxatilis (Striped bass).
Q90WC9;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Perciformes; Parcoidei; Moronidae; Morone.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Perciformes; Parcoidei; Moronidae; Morone.
Q90WC9;	RN	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
Q90WC9;	RC	TISSUE=SKELETAL_MUSCLE;	TISSUE=SKELETAL_MUSCLE;
Q90WC9;	RX	MEDLINE=21292680; PubMed=11399495;	MEDLINE=21292680; PubMed=11399495;
Q90WC9;	RA	Rodgers B.D., Weber G.M.;	Rodgers B.D., Weber G.M.;
Q90WC9;	RT	"Sequence conservation among fish myostatin orthologues and the characterization of two additional cDNA clones from <i>Morone saxatilis</i> and <i>Morone americana</i> .";	"Sequence conservation among fish myostatin orthologues and the characterization of two additional cDNA clones from <i>Morone saxatilis</i> and <i>Morone americana</i> .";
Q90WC9;	DR	Comp. Biochem. Physiol. B. Biochem. Mol. Biol. 129:597-603 (2001).	Comp. Biochem. Physiol. B. Biochem. Mol. Biol. 129:597-603 (2001).
Q90WC9;	DR	EMBL: AF250910; AAK67983_1; -	EMBL: AF250910; AAK67983_1; -
Q90WC9;	SQ	SEQUENCE 376 AA; 42794 MW; E2C5D61FF27DBA14 CRC64;	SEQUENCE 376 AA; 42794 MW; E2C5D61FF27DBA14 CRC64;
Q90WC8	PRELIMINARY;	Q90WC8;	Q90WC8;
Q90WC8;	PRT; 376 AA.	Q90WC8;	Q90WC8;
Q90WC8;	RT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
Q90WC8;	DR	MYOSTATIN.	MYOSTATIN.
Q90WC8;	OS	Morone americana (White perch).	Morone americana (White perch).
Q90WC8;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Perciformes; Parcoidei; Moronidae; Morone.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Perciformes; Parcoidei; Moronidae; Morone.
Q90WC8;	RN	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
Q90WC8;	RC	TISSUE=SKELETAL_MUSCLE;	TISSUE=SKELETAL_MUSCLE;
Q90WC8;	RA	MEDLINE=21150052; PubMed=11250920;	MEDLINE=21150052; PubMed=11250920;
Q90WC8;	RT	"Isolation and Characterization of Myostatin Complementary DNA Clones from Two Commercially Important Fish: <i>Oreochromis mossambicus</i> and <i>Morone chrysops</i> .";	"Isolation and Characterization of Myostatin Complementary DNA Clones from Two Commercially Important Fish: <i>Oreochromis mossambicus</i> and <i>Morone chrysops</i> .";
Q90WC8;	DR	Endocrinology 142:1412-1418 (2001).	Endocrinology 142:1412-1418 (2001).
Q90WC8;	DR	-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.	-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
Q90WC8;	DR	HSSP: P12643; B2MP.	HSSP: P12643; B2MP.
Q90WC8;	DR	InterPro: IPR01839; TGF-beta.	InterPro: IPR01839; TGF-beta.
Q90WC8;	DR	IntePro: IPR01111; TGFb_N.	IntePro: IPR01111; TGFb_N.
Q90WC8;	DR	Pfam: PF00019; TGF-beta; 1.	Pfam: PF00019; TGF-beta; 1.
Q90WC8;	DR	Pfam: PF00688; TGFb_propeptide; 1.	Pfam: PF00688; TGFb_propeptide; 1.
Q90WC8;	DR	Prodom: P000357; TGF-beta; 1.	Prodom: P000357; TGF-beta; 1.
Q90WC8;	DR	SMART: SM00204; TGFb; 1.	SMART: SM00204; TGFb; 1.
Q90WC8;	DR	PROSITE: PS00250; TGF_beta; 1.	PROSITE: PS00250; TGF_beta; 1.
Q90WC8;	DR	Glycoprotein.	Glycoprotein.
Q90WC8;	SQ	SEQUENCE 376 AA; 42550 MW; TC3469D1314B01E6 CRC64;	SEQUENCE 376 AA; 42550 MW; TC3469D1314B01E6 CRC64;
QY	1 DFGLCDDEHTESRCRCRYPTLVDFAFGWMWIAPIRKYKANYCSCGCEFFVFLQKYPHTHL 60	Db	268 DSGLCDENSPESRCRYPTLVDFFGWMWIAPIRKYKANYCSCGCEYMLQKYPHTHL 327
Q90WC8	PRELIMINARY;	Q90WC8;	Q90WC8;
Q90WC8;	PRT; 376 AA.	Q90WC8;	Q90WC8;
Q90WC8;	RT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
Q90WC8;	DR	MYOSTATIN.	MYOSTATIN.
Q90WC8;	OS	Morone saxatilis (Striped bass).	Morone saxatilis (Striped bass).
Q90WC8;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Perciformes; Parcoidei; Moronidae; Morone.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Perciformes; Parcoidei; Moronidae; Morone.
Q90WC8;	RN	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
Q90WC8;	RC	TISSUE=SKELETAL_MUSCLE;	TISSUE=SKELETAL_MUSCLE;
Q90WC8;	RA	Rodgers B.D., Weber G.M.;	Rodgers B.D., Weber G.M.;
Q90WC8;	RT	"Sequence conservation among fish myostatin orthologues and the characterization of two additional cDNA clones from <i>Morone saxatilis</i> and <i>Morone americana</i> .";	"Sequence conservation among fish myostatin orthologues and the characterization of two additional cDNA clones from <i>Morone saxatilis</i> and <i>Morone americana</i> .";
Q90WC8;	DR	Comp. Biochem. Physiol. B. Biochem. Mol. Biol. 129:597-603 (2001).	Comp. Biochem. Physiol. B. Biochem. Mol. Biol. 129:597-603 (2001).

DR EMBL: AF290911; AAK67984; . . .  
SQ SEQUENCE 376 AA; 42779 MW; 9CC57A5444A7E5E8 CRC64;

Query	Match	Score	DB	Length
Best Local Similarity	88.7%	557	13	376
Matches	96	Conservative	6	0
Oy	1	DRLGDCDCEHSTSSRCCRPLVTFEARFGWDWLTAPKRYKANYCSGECCEVFLOKYPHTHL	60	0
Db	268	DSGLCDCDENSPESRCRPLVTFEDFGWDWLTAPKRYKANYCSGECCEVFLOKYPHTHL	60	327
Oy	61	VIQANPQGSGACGCTPLMSPINLYFNGKEQIYGKIPAMWDRCGGS	109	109
Db	328	VNKANPQRTAGCCTPTKMSPINLYFNGKEQIYGKIPAMWDRCGGS	376	376

Search completed: May 20, 2002, 09:24:32  
Job time: 222 sec

גנום לריאו





A;Title: Activin B: precursor sequences, genomic structure and in vitro activities.  
 A;Reference number: A40150; MUID:90114200  
 A;Accession: A40150  
 A;Molecule type: DNA  
 A;Residues: 1-407 <MASS>  
 R;Mason, A.J.; Niall, H.D.; Seeburg, P.H.; Biochem. Biophys. Res. Commun. 135, 957-964, 1986  
 A;Title: Structure of two human ovarian inhibins.  
 A;Reference number: A90123; MUID:86186863  
 A;Accession: C24248  
 A;Molecule type: mRNA  
 A;Residues: 55-407 <MASS>  
 A;Cross-references: GB:M31668; GR:M31669; NID:9186419; PIDN:AAA59451.1; PID:9386827  
 R;Feng, Z.M.; Bardin, C.W.; Chen, C.L.C.; Mol. Endocrinol. 3, 939-948, 1989  
 A;Title: Characterization and regulation of testicular inhibin beta-subunit mRNA.  
 A;Reference number: A40156; MUID:89205443  
 A;Accession: A40156  
 A;Molecule type: mRNA  
 A;Residues: 22-46; A' 48-407 <FEN>  
 A;Cross-references: GB:M31632  
 A;Experimental source: testis  
 A;Schmeidler, C.H.; Burton, L.E.; Tamony, C.M.; Schwall, R.H.; Mason, A.J.; Liegeois, N.; Blochim. Biophys. Acta 1039, 135-141, 1990  
 A;Title: Purification and characterization of recombinant human activin B.  
 A;Reference number: S10751; MUID:90304183  
 A;Accession: S10751  
 A;Molecule type: protein  
 A;Residues: 293-294, 'GX', 297-302, 'XX', 305-307 <SCH>  
 C;Comment: Activins A and B are homodimers of inhibin beta-A or inhibin beta-B, respectively.  
 C;Genetics:  
 A;Gene: GDB:INHB  
 A;Cross-references: GDB:119347; OMIM:147390  
 A;Map position: 2cen-2q13  
 C;Superfamily: inhibin  
 C;Keywords: glycoprotein; gonad; heterodimer; homodimer; hormone  
 F;1-20/Domain: signal sequence #status predicted <SIC>  
 F;21-292/Domain: propertide #status predicted <PRO>  
 F;293/Product: inhibin beta-B chain #status predicted <MAT>  
 F;293/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 37.4%; Score 235; DB 1; Length 407;  
 Best Local Similarity 39.8%; Pred. No. 7e-18;  
 Matches 47; Conservative 18; Mismatches 39; Indels 14; Gaps 5;  
 QY 3 GLDCDEHSTESRCRCRYPTDVFEEAFGW-DWIIAPKRYKANYSGECCEVFVLOKYP---- 56  
 Db 294 GLDCDGRY--NUCCROOFFIDFRLIGWWDIIAPTYGGINCEGSCC-AVYLAGVPSASS 350  
 QY 57 -HHLVHQANPR---GSAGPCCTPLMSPINMLYNGKEQIYKGIPAMVWDRCCGS 109  
 Db 351 FHTAVVNOYRMGLNPGTIVNSCCIPKTLSMSLYFDDENIVKRDVPMIVECGCA 408  
 RESULT 8  
 I50103  
 Activin beta B - zebra fish  
 C;Species: Brachydanio rerio (zebra fish)  
 C;Accession: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Jul-1999  
 R;Wittbrodt, J.; Rosa, F.M.; Genes Dev. 8, 1448-1462, 1994  
 A;Title: Disruption of mesoderm and axis formation in fish by ectopic expression of a  
 A;Reference number: I50103; MUID:95011555  
 A;Accession: I50103  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-393 <WIT>  
 A;Cross-references: EMBL:X76051; NID:9516356; PIDN:CAA53636.1; PID:9516357  
 C;Genetics:  
 A;Gene: ZactbetaB  
 A;Map position: 2cen-2q13  
 C;Superfamily: inhibin  
 Query Match 37.3%; Score 234.5; DB 2; Length 393;  
 Best Local Similarity 39.8%; Pred. No. 7e-18;  
 Matches 47; Conservative 18; Mismatches 40; Indels 13; Gaps 5;  
 QY 3 GLDCDEHSTESRCRCRYPTDVFEEAFGW-DWIIAPKRYKANYSGECCEVFVLOKYP---- 56  
 Db 278 GLDCDGNN-GGLCCRQQFYIDFRLIGWWDIIAPAGYYGNYCEGSCP-AYMAGVPGSASS 335  
 QY 57 -HHLVHQANPR---GSAGPCCTPLMSPINMLYNGKEQIYKGIPAMVWDRCCGS 109  
 Db 336 FHTAVVNOYRMGLNPGTIVNSCCIPKTLSMSLYFDDENIVKRDVPMIVECGCA 393  
 RESULT 9  
 PNO505  
 activin beta B-1 chain - goldfish (fragment)  
 N;Alternate names: gact, 2  
 C;Species: Carassius auratus (goldfish)  
 C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
 C;Accession: PNO505  
 R;Ge, W.; Gallin, W.J.; Strobeck, C.; Peter, R.E.; Biochem. Biophys. Res. Commun. 133, 711-717, 1983  
 A;Title: Cloning and sequencing of goldfish activin subunit genes: Strong structural  
 A;Reference number: PNO504; MUID:93290666  
 A;Accession: PNO505  
 A;Molecule type: DNA  
 A;Residues: 1-115 <GEW>  
 C;Superfamily: inhibin  
 Query Match 37.0%; Score 232.5; DB 2; Length 115;  
 Best Local Similarity 40.2%; Pred. No. 3.6e-18;  
 Matches 47; Conservative 16; Mismatches 41; Indels 13; Gaps 5;  
 QY 3 GLDCDEHSTESRCRCRYPTDVFEEAFGW-DWIIAPKRYKANYSGECCEVFVLOKYP---- 56

RESULT 7  
 S50899  
 becAB inhibin precursor - bovine  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 01-Aug-1995 #sequence\_revision 01-Sep-1995 #text\_change 17-Mar-1999  
 C;Accession: S50899  
 R;Thompson, D.A.; Cronin, C.N.; Martin, F.; Eur. J. Biochem. 226, 751-764, 1994  
 A;Title: Genomic cloning and sequence analyses of the bovine alpha-, beta(A)- and beta(B)  
 Y;DNase I footprinting  
 A;Reference number: S50897; MUID:95112839  
 A;Accession: S50899  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-408 <THO>  
 A;Cross-references: EMBL:U16240

RESULT 10

S37618 Query Match 35.9%; Score 225.5; DB 2; Length 513; Best Local Similarity 41.4%; Pred. No. 9.7e-17; Matches 46; Conservative 13; Mismatches 45; Indels 7; Gaps 2; C:Species: Rattus norvegicus (Norway rat) C;Date: 18-Feb-1994 #sequence\_revision 26-May-1995 #text\_change 16-Jul-1999 C;Accession: S37618 R;Sauermann, U.; Meiermann, R.; Schliuener, H.J. J. Neurosci. Res. 33, 142-147, 1992 A;Title: Cloning of a novel TGF-beta related cytokine, the vgr, from rat brain: cloning A;Reference number: 537618; MUID:93085738 A;Status: preliminary A;Molecule type: mRNA A;Cross-references: EMBL:X58830; NID:957475; PIDN:CAA1634.1; PID:957476 A;Note: the sequence from Fig. 4 is inconsistent with that from Fig. 1 in having 88-Ser;Superfamily: inhibin

RESULT 11

BMH6 Query Match 35.9%; Score 225.5; DB 2; Length 207; Matches 46; Conservative 13; Mismatches 45; Indels 7; Gaps 2; C:Species: Homo sapiens (man) C;Date: 18-Oct-1991 #sequence\_revision 03-Aug-1995 #text\_change 18-Jun-1999 C;Accession: B30263 R;Celeste, A.J.; Iannuzzi, J.A.; Taylor, R.C.; Hewick, R.M.; Rosen, V.; Wang, E.A.; Wozniak, M.; Molecular type: mRNA R;Title: Identification of transforming growth factor beta family members present in bone morphogenetic protein 6 precursor - human A;Reference number: A39263; MUID:91088608 A;Accession: B30263 A;Cross-references: GB:M60315; GB:M38694; NID:9339561; PIDN:AAA36737.1; PID:9339562 A;Genetics: GDB: BMP6 A;Gene: GDB: BMP6 A;Cross-references: GDB:127596; OMIM:112266 A;Map position: 6pter-6qter C;Superfamily: Inhibin C;Keywords: bone; glycoprotein F;1-27/Domain; signal sequence #status predicted <SIG> F;24-374/Domain; propeptide #status predicted <PRO> F;375-513/Product; bone morphogenetic protein 6 #status predicted <MAT> F;241-269,386,404,454/Binding site: carbohydrate (Asn) (covalent) #status predicted

RESULT 12

QY 57 Query Match 35.9%; Score 225.5; DB 2; Length 513; Best Local Similarity 41.4%; Pred. No. 9.7e-17; Matches 46; Conservative 13; Mismatches 45; Indels 7; Gaps 2; C:Species: Rattus norvegicus (Norway rat) C;Date: 18-Feb-1994 #sequence\_revision 26-May-1995 #text\_change 16-Jul-1999 C;Accession: S37618 R;Sauermann, U.; Meiermann, R.; Schliuener, H.J. J. Neurosci. Res. 33, 142-147, 1992 A;Title: Cloning of a novel TGF-beta related cytokine, the vgr, from rat brain: cloning A;Reference number: 537618; MUID:93085738 A;Status: preliminary A;Molecule type: mRNA A;Cross-references: EMBL:X58830; NID:957475; PIDN:CAA1634.1; PID:957476 A;Note: the sequence from Fig. 4 is inconsistent with that from Fig. 1 in having 88-Ser;Superfamily: inhibin

RESULT 13

QY 60 Query Match 35.6%; Score 223.5; DB 2; Length 510; Best Local Similarity 41.4%; Pred. No. 1.6e-16; Matches 46; Conservative 13; Mismatches 45; Indels 7; Gaps 2; C:Species: Mus musculus (house mouse) C;Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 16-Jul-1999 C;Accession: A54798 R;Gitelman, S.E.; Kobrin, M.S.; Ye, J.Q.; Lopez, A.R.; Lee, A.; Deryck, R. J. Cell Biol. 126, 1159-1169, 1994 A;Title: Recombinant vgr-1, a BMU-6-expressing tumors induce fibrosis and endochondral b A;Reference number: A54798; MUID:943753 A;Status: preliminary A;Accession: A54798 A;Molecule type: mRNA A;Cross-references: EMBL:X80932; NID:9530729; PIDN:CAA56917.1; PID:9530730 R;Lyons, K.; Graycar, J.L.; Lee, A.; Hashmi, S.; Lindquist, P.B.; Chen, E.Y.; Hogan, Proc. Natl. Acad. Sci. U.S.A. 86, 4554-4558, 1989 A;Title: vgr-1, a mammalian gene related to Xenopus vg-1, is a member of the transfor A;Reference number: A33925; MUID:89282810 A;Accession: A33925 A;Status: preliminary A;Molecule type: mRNA A;Cross-references: GB:J04566; NID:9202352; PIDN:AAA40548.1; PID:9202353 A;Cross-references: GB:J04566; NID:9202352; PIDN:AAA40548.1; PID:9202353 C;Superfamily: inhibin

RESULT 14

QY 96 Query Match 35.6%; Score 223.5; DB 2; Length 510; Best Local Similarity 41.4%; Pred. No. 1.6e-16; Matches 46; Conservative 13; Mismatches 45; Indels 7; Gaps 2; C:Species: Gallus gallus (chicken) C;Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 16-Jul-1999 C;Accession: B30263 R;Houston, B.; Thorp, B.H.; Burt, D.W. J. Mol. Endocrinol. 13, 289-301, 1994 A;Title: Molecular cloning and expression of bone morphogenetic protein-7 in the chick A;Reference number: 151284; MUID:95200473 A;Accession: 151284 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-313 <HOU> A;Cross-references: GB:S77477; NID:957233; PIDN:AB33846.1; PID:957234 C;Superfamily: inhibin

RESULT 15

QY 462 Query Match 33.8%; Score 212.5; DB 2; Length 313; Best Local Similarity 40.3%; Pred. No. 1.5e-15; Matches 48; Conservative 14; Mismatches 44; Indels 13; Gaps 5; C:Species: Mus musculus (house mouse) C;Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 16-Jul-1999 C;Accession: A54798 R;Gitelman, S.E.; Kobrin, M.S.; Ye, J.Q.; Lopez, A.R.; Lee, A.; Deryck, R. J. Cell Biol. 126, 1159-1169, 1994 A;Title: Recombinant vgr-1, a BMU-6-expressing tumors induce fibrosis and endochondral b A;Reference number: A54798; MUID:943753 A;Status: preliminary A;Accession: A54798 A;Molecule type: mRNA A;Cross-references: EMBL:X80932; NID:9530729; PIDN:CAA56917.1; PID:9530730 R;Lyons, K.; Graycar, J.L.; Lee, A.; Hashmi, S.; Lindquist, P.B.; Chen, E.Y.; Hogan, Proc. Natl. Acad. Sci. U.S.A. 86, 4554-4558, 1989 A;Title: vgr-1, a mammalian gene related to Xenopus vg-1, is a member of the transfor A;Reference number: A33925; MUID:89282810 A;Accession: A33925 A;Status: preliminary A;Molecule type: mRNA A;Cross-references: GB:J04566; NID:9202352; PIDN:AAA40548.1; PID:9202353 A;Cross-references: GB:J04566; NID:9202352; PIDN:AAA40548.1; PID:9202353 C;Superfamily: inhibin

RESULT 16

QY 195 Query Match 33.8%; Score 212.5; DB 2; Length 313; Best Local Similarity 40.3%; Pred. No. 1.5e-15; Matches 48; Conservative 14; Mismatches 44; Indels 13; Gaps 5; C:Species: Gallus gallus (chicken) C;Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 16-Jul-1999 C;Accession: B30263 R;Houston, B.; Thorp, B.H.; Burt, D.W. J. Mol. Endocrinol. 13, 289-301, 1994 A;Title: Molecular cloning and expression of bone morphogenetic protein-7 in the chick A;Reference number: 151284; MUID:95200473 A;Accession: 151284 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-313 <HOU> A;Cross-references: GB:S77477; NID:957233; PIDN:AB33846.1; PID:957234 C;Superfamily: inhibin

RESULT 17

QY 57 Query Match 33.8%; Score 212.5; DB 2; Length 313; Best Local Similarity 40.3%; Pred. No. 1.5e-15; Matches 48; Conservative 14; Mismatches 44; Indels 13; Gaps 5; C:Species: Gallus gallus (chicken) C;Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 16-Jul-1999 C;Accession: B30263 R;Houston, B.; Thorp, B.H.; Burt, D.W. J. Mol. Endocrinol. 13, 289-301, 1994 A;Title: Molecular cloning and expression of bone morphogenetic protein-7 in the chick A;Reference number: 151284; MUID:95200473 A;Accession: 151284 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-313 <HOU> A;Cross-references: GB:S77477; NID:957233; PIDN:AB33846.1; PID:957234 C;Superfamily: inhibin

Db 254 NATNHATVOTLVHFINPETVPKPCAPTOQNALISVLYFDDSSNVILKRYRNWVRACGC 312

RESULT 14

A29619 ||| embryonic growth factor - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 21-Jul-2000

C:Accession: A29619

R:Weeks, D.L.; Melton, D.A.

Cell 51, 861-867, 1987

A:Title: A maternal mRNA localized to the vegetal hemisphere in Xenopus eggs codes for a

A:Reference number: A29619; MUID:88052889

A:Accession: A29619

A:Molecule type: mRNA

A:Residues: 1-360 <WEB>

C:Cross-references: GB: M18055; NID:9214179; PIDN:AAA49727.1; PID:9214180

C:Keywords: inhibin

C:Keywords: growth factor

Query Match 33.8%; Score 212.5; DB 2; Length 360;  
 Best Local Similarity 39.3%; Pred. No. 1.8e-15; Mismatches 33; Indels 19; Gaps 3;  
 Matches 42; Conservative 13;

Qy 15 CCKRYPLTVDFEAFGM-DWIIAPKRKYKANYCSCGECEFVFLQKY-PHTH-----LV 61  
 Db 259 CKKRRHLVKEFKDVGWQWNVIAPQGYMANCYGEC-----PYPLTEILNGSNHAILQTLV 312

Qy 62 HQANPQPSAGPCTPTMSPTIMSPINMLYFNGKEQIYGKIPAMVYDRCGC 108  
 Db 313 HSEPEDEDIPLPCCVPTKMSPISMLFYDNNDNVVLRHYENMAVDECGC 359

RESULT 15

S43295 bone morphogenetic protein homolog GDF6 precursor - mouse (fragment)

N:Alternative names: growth and differentiation factor 6

C:Species: Mus musculus (house mouse)

C:Date: 20-oct-1994 #sequence\_revision 07-Feb-1997 #text\_change 26-May-2000

C:Accession: S43295

R:Storm, E.E.; Huihnh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.

A:Title: Limb alterations in brachyopodism mice due to mutations in a new member of the T

A:Reference number: S43294; MUID:94195427

A:Accession: S43295

A:Molecule type: DNA

A:Residues: 1-125 <STO>

A:Cross-references: EMBL:U08338; NID:9488463; PIDN:AAA18779.1; PID:9488464

C:Genetics:

C:Gene: Gdf6

C:Superfamily: inhibin

F:1-5/domain: polybasic protease recognition site #status predicted <PPR>

F:6-125/Product: bone morphogenetic protein homolog GDF6 (fragment) #status predicted <M

Query Match 33.7%; Score 211.5; DB 2; Length 125;  
 Best Local Similarity 38.5%; Pred. No. 7.6e-16; Mismatches 39; Indels 9; Gaps 4;  
 Matches 42; Conservative 19; Mismatches 39; Indels 9; Gaps 4;

Qy 9 HSPES - -RCCRYPLTVDFEAFGM-DWIIAPKRKYKANYCSCGECEFVFLQKY-PHTH----- 59  
 Db 16 HGRKSRRLRCRSPKHLVNEKELGWDWIIAPLEYAVHCEGWDPLRSHEPNTNHAITQ 75

Qy 60 LVMQANPQPSAGPCTPTMSPTIMSPINMLYFNGKEQIYGKIPAMVYDRCGC 108  
 Db 76 LMNSMDPGSTPPSCCVPTKLTPIISLYDAGNNWVYQYEDMVYESC 124

Search completed: May 20, 2002, 09:21:10

Job time: 45 sec

Mon May 20 09:12:37 2002

us-09-754-826-2.rpr



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model.

Run on:

May 20, 2002, 09:20:25 ; Search time 30.38 Seconds

(without alignments)  
398.520 Million cell updates/sec

Title:

US-09-754-826-2

Perfect score:

628  
1 DFGIDCDEHSTESRCCRYPL.....KEQIYKGKPAWMVDRCCS 109

Sequence:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Scoring table:

747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters:

747574

Minimum DB seq length:

0

Maximum DB seq length:

2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_032802:\*

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2: /SIDS1/gcadata/hold-geneseq/geneseqp-emb1/AA1981.DAT:\*

3: /SIDS1/gcadata/hold-geneseq/geneseqp-emb1/AA1982.DAT:\*

4: /SIDS1/gcadata/hold-geneseq/geneseqp-emb1/AA1983.DAT:\*

5: /SIDS1/gcadata/hold-geneseq/geneseqp-emb1/AA1984.DAT:\*

6: /SIDS1/gcadata/hold-geneseq/geneseqp-emb1/AA1985.DAT:\*

7: /SIDS1/gcadata/hold-geneseq/geneseqp-emb1/AA1987.DAT:\*

8: /SIDS1/gcadata/hold-geneseq/geneseqp-emb1/AA1988.DAT:\*

9: /SIDS1/gcadata/hold-geneseq/geneseqp-emb1/AA1989.DAT:\*

10: /SIDS1/gcadata/hold-geneseq/geneseqp-emb1/AA1990.DAT:\*

11: /SIDS1/gcadata/hold-geneseq/geneseqp-emb1/AA1991.DAT:\*

12: /SIDS1/gcadata/hold-geneseq/geneseqp-emb1/AA1992.DAT:\*

13: /SIDS1/gcadata/hold-geneseq/geneseqp-emb1/AA1993.DAT:\*

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15: /SIDS1/gcadata/hold-geneseq/geneseqp-emb1/AA1995.DAT:\*

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22: /SIDS1/gcadata/hold-geneseq/geneseqp-emb1/AA2002.DAT:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

\* Query

No. Score Match length DB ID

Description

RESULT 1

ID AAB20141 standard; Protein; 109 AA.

XX AAB20141; AC

XX 30-APR-2001 (first entry)

DE Human growth differentiation factor 8 C-terminal region.

XX Growth differentiation factor 8; GDF-8; myostatin; down-regulation;

KW vaccine; muscle; meat; cachexia; cardiant; human; mutant; mutein.

XX Homo sapiens.

OS Synthetic.

XX WO200105820-A2.

XX 25-JAN-2001.

\* Query

No. Score Match length DB ID

Description

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XX AAB20141; AC

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XX Homo sapiens.

OS Synthetic.

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XX 25-JAN-2001.

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Description

RESULT 1

ID AAB20141 standard; Protein; 109 AA.

XX AAB20141; AC

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XX Homo sapiens.

OS Synthetic.

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XX 25-JAN-2001.

\* Query

No. Score Match length DB ID

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RESULT 1

ID AAB20141 standard; Protein; 109 AA.

XX AAB20141; AC

XX 30-APR-2001 (first entry)

DE Human growth differentiation factor 8 C-terminal region.

XX Growth differentiation factor 8; GDF-8; myostatin; down-regulation;

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XX Homo sapiens.

OS Synthetic.

XX WO200105820-A2.

XX 25-JAN-2001.

\* Query

No. Score Match length DB ID

Description

RESULT 1

ID AAB20141 standard; Protein; 109 AA.

XX AAB20141; AC

XX 30-APR-2001 (first entry)

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XX Homo sapiens.

OS Synthetic.

XX WO200105820-A2.

XX 25-JAN-2001.

\* Query

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Description

RESULT 1

ID AAB20141 standard; Protein; 109 AA.

XX AAB20141; AC

XX 30-APR-2001 (first entry)

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XX Homo sapiens.

OS Synthetic.

XX WO200105820-A2.

XX 25-JAN-2001.

\* Query

No. Score Match length DB ID

Description

RESULT 1

ID AAB20141 standard; Protein; 109 AA.

XX AAB20141; AC

XX 30-APR-2001 (first entry)

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XX 25-JAN-2001.

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XX AAB20141; AC

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XX AAB20141; AC

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Claim 17; Page 93-94; 110pp; English.

claim 17; Page 93-94; 110pp; English.

The present sequence comprises the 109 amino acid residue C-terminal region of human differentiation factor 8 (GDF-8), i.e. residues 267-375 of the full-length protein (see NAB20131). The homodimer of this region is thought to be the biologically active form of GDF-8. It is an object of the invention to produce a recombinant therapeutic vaccine capable of effecting down-regulation of GDF-8 in order to increase the muscle growth rate of farm animals. Variants of GDF-8 (see NAB20145-53) are provided that are capable of breaking autotolerance against autologous GDF-8. These comprise the C-terminal portion of human GDF-8 in which a portion of the native sequence is replaced by a T-cell epitope such as the promiscuous tetanus toxin T-cell epitope p2 or p20. The high number (9) of Cys residues in the C-terminal region limits the possible sites in which the T-cell epitope can be positioned without major disturbance of the native 3-dimensional structure of the protein. Nucleic acids encoding the GDF-8 variants can be used for genetic immunisation of the animals. Down regulation of GDF-8 activity can increase muscle mass by up to at least 45% in cattle, pigs and poultry used for meat production, reducing the need for antibiotic feed-additives. Anti-GDF-8 vaccines can be used to treat human diseases such as cancer cachexia where muscle atrophy is pronounced and for patients suffering from acute and chronic heart

XX  
SQ Sequence 109 AA;

Query Match	99.0%	Score 622;	DB 22;	Length 109;
Best Local Similarity	99.1%	Pred. No.	1. 3e-59;	
Matches 108; Conservative	0;	Mismatches	1;	Indels 0;
				Gaps 0

Query	Match	Score	DB	Length
Qy	Query	99.0%	DB 22;	Length 10
Db	Best local Similarity	99.1%	Pred. No. 1.	3e-59;
Qy	Matches	108;	Conservative	0;
Db	Missmatches	1;	Indels	
Qy	1	DFGLCDCEHISTESRCRCRYPLTVDEBAFGMDWIAIPKRYKANCSECEFVLQQ		
Db	1	dfgldcdehistescrcrypltvdeafgmdwiaipkrykancsecefflq		
Qy	61	VHQANPRGSSAGPCCPMTLSPINMLYENKEQITYKGKIPAMVNDRGCS	109	
Db	61	vhqanprssagpcptkmspnlyfnqkeiqiykgkiamvdccgs	109	

RESULT	2
ID	AAR63161
XX	AAR63161 standard; Protein; 126 AA
AC	AAR63161:
XX	
DT	23-JUN-1995 (first entry)

Mouse growth differentiation factor-8 partial sequence.  
Growth differentiation factor-8; GDF-8; Cell proliferation  
adipocyte; obesity; transforming growth factor-beta.

WO9421681-A.

18-MAR-1994; 94WO-US03019.

19-MAR-1993; 930S-0033923.

Mr. S. McPherron AG: (UYJO) UNIV JOHNS HOPKINS SCHOOL MED.

49PT; 1994-316943/39  
O-PSDB: 076380

PT	New growth differentiation factor 8 - useful for treatment and diagnosis of cell proliferative disorders esp. of muscle.
XX	
PS	Disclosure; Page 41; 84pp; English.
XX	
CC	GDF-8 can be used to maintain cells before transplantation; to improve efficiency of cell fusion and to treat obesity or diseases related to abnormal adipocyte proliferation.
CC	
CC	biologically active form of GDF-8. It is an object of the invention to produce a recombinant therapeutic vaccine capable of effecting down-regulation of GDF-8 in order to increase the muscle growth rate of farm animals. Variants of GDF-8 (see AB20145-53) are provided that are capable of breaking autotolerance against autologous GDF-8. These comprise the C-terminal portion of human GDF-8 in which a portion of the native sequence is replaced by a T-cell epitope such as the promiscuous tetanus toxin T-cell epitope P2 or P30. The high number (9) of Cys residues in the C-terminal region limits the possible sites in which the T-cell epitope can be positioned without major disturbance of the native 3-dimensional structure of the protein. Nucleic acids encoding the GDF-8 variants can be used for genetic immunisation of the animals. Down-regulation of GDF-8 activity can increase muscle mass by up to at least 45% in cattle, pigs and poultry used for meat production, reducing the need for antibiotic feed-additives. Anti-GDF-8 vaccines can be used to treat human diseases such as cancer, cachexia, where muscle atrophy is pronounced and for patients suffering from acute and chronic heart failure.
CC	
CC	GDF-8 in which a portion of the native sequence is replaced by a T-cell epitope such as the promiscuous tetanus toxin T-cell epitope P2 or P30. The high number (9) of Cys residues in the C-terminal region limits the possible sites in which the T-cell epitope can be positioned without major disturbance of the native 3-dimensional structure of the protein. Nucleic acids encoding the GDF-8 variants can be used for genetic immunisation of the animals. Down-regulation of GDF-8 activity can increase muscle mass by up to at least 45% in cattle, pigs and poultry used for meat production, reducing the need for antibiotic feed-additives. Anti-GDF-8 vaccines can be used to treat human diseases such as cancer, cachexia, where muscle atrophy is pronounced and for patients suffering from acute and chronic heart failure.
XX	
SQ	Sequence 109 AA;
XX	
Query Match	99.0%; Score 622; DB 22; Length 109;
Best Local Similarity	99.1%; Pred. No. 1.3e-59; DB 22; Length 109;
Matches	108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 DFGIDCDEHSTESTRCCRPLTVDFEAGFDWDTIAPKRYKANCSGCECFVFLQKYPHHL 60
Db	1 dfgidcdehstestrccrpltvafeagfdwldiakrykanycsgeefvfifqkyphhl 77
QY	61 VHQANPRGSAGPCCPTLMSPINLYFNGKEQIYKGKIPAMVWDRCCS 109
Db	78 vhqanprgsagpccptkmspimlyfngkeqiykgkipamvvdrcgcs 126
Db	61 vhqanprgsagpccptkmspimlyfngkeqiykgkipamvvdrcgcs 109
Db	61 vhqanprgsagpccptkmspimlyfngkeqiykgkipamvvdrcgcs 109
Db	61 vhqanprgsagpccptkmspimlyfngkeqiykgkipamvvdrcgcs 109
RESULT	2
AR63161	TD AAR63161 standard; Protein; 126 AA.
XX	
AC	AAR63161:
XX	
DT	07-DEC-1998 (first entry)
XX	
DE	Murine growth differentiation factor-8 C-terminal fragment.
XX	
KW	Growth differentiation factor-8; GDF-8; mouse; transgenic animal; transforming growth factor-beta; muscle; meat; inhibitor; obesity; neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer; therapy.
XX	
OS	Mus sp.
XX	
FT	Key
FT	Cleavage-site 13..14
FT	Cleavage-site 16..17
FT	Protein 17..125
FT	/note= "mature polypeptide"
XX	
PN	W09833887-A1.
XX	
PD	06-AUG-1998.
XX	
PF	05-FEB-1998; 98WO-US02479.
XX	
PR	23-MAY-1997; 97US-082445.
PR	05-FEB-1997; 97US-0795071.
PR	28-APR-1997; 97US-0847910.
XX	
PA	(UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX	
PI	Lee S, McPherron AC;
XX	
DR	WPI: 1998-437444/37.
DR	N-PSDB; NAV45809.
XX	
PT	Transgenic animals with gene for growth differentiation factor-8 disrupted - have increased muscle and reduced cholesterol contents, also use of GDF-8 inhibitors for treating cancer, obesity, neuromuscular disease
PT	
PS	Example 2; Page 58; 125pp; English.
XX	
CC	This is the amino acid sequence of the C-terminal portion of mouse

CC growth differentiation factor-8 (GDF-8), a novel member of the  
 CC transforming growth factor-beta superfamily that appears to relate  
 CC to various cell proliferative disorders, especially those involving  
 CC muscle, nerve and adipose tissue. The sequence was deduced from a  
 CC partial genomic clone (see AAV5809). A full-length sequence (see  
 CC AAW30889) has been deduced from a cDNA clone (see AAV4213). The  
 CC invention provides novel mammalian and avian GDF-8 proteins (see  
 CC AAW69833-92). A transgenic non-human animal is claimed in which  
 CC, GDF-8 expression is disrupted or interfered with. Also claimed  
 are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb  
 from these animals; (2) method for increasing muscle mass in  
 CC animals by administering an antibody (Ab) that binds to GDF-8; (3)  
 CC inhibiting the action of GDF-8 by treating foetal or adult muscle  
 CC or progenitor cells with a GDF-8 inhibitor; (4) isolated nucleic  
 CC acid encoding a GDF-8 protein truncated by loss of the C-terminal  
 CC active fragment. The transgenic animals have increased muscle mass  
 and for poultry reduced cholesterol contents. Method (3) is used  
 to treat muscle wasting or neuromuscular diseases, muscular atrophy  
 and aging, particularly muscular dystrophy, spinal cord or  
 CC traumatic injuries, congestive or obstructive lung disease, AIDS  
 CC and cachexia. Method (4) is used to treat cancer of muscle,  
 CC connective tissue and bone, or obesity. Also (not claimed) GDF-8  
 can be used to maintain myoblasts intended for transplanting or to  
 CC improve efficiency of fusion. Ab can be used to detect and  
 CC quantify GDF-8 (particularly in muscle, for diagnosis or monitoring),  
 CC also for immunotherapy and in vivo imaging.  
 SQ Sequence 126 AA;

Query Match 99.0%; Score 622; DB 19; Length 126;  
 Best Local Similarity 99.1%; Pred. No. 1; 6e-59; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DRGLCDEHSTESRCRCPYPLTVDFEARFQWDMWIAPKRYKANYCSGCECFVFLQKYPTHL 60  
 Db 18 df91dcdehstesrcrccrypltvdfefagfdwjiapkrykanycsgecefvlqkyphthl 77

Oy 61 VHQANPRGSAGCCTPLMSPINMLYFNGKQOIYKRYKIPAMVDRGCS 109  
 Db 78 vhqanprgsagcctplkmspinmlyfngkeqilqykipamvdrqcs 126

RESULT 4  
 AAY1586 D AAY1586 standard; Protein: 126 AA.

AC AAY1586;  
 XX DT 08-DEC-1999 (first entry)

XX DE C-terminal region of mouse Growth Differentiation Factor-8 (GDF-8).  
 XX

KW growth differentiation factor; tissue growth; muscle growth;  
 KW cell differentiation; animal; feed; muscle disorder;  
 KW bone degeneration; nerve degeneration; GDF-8; development;  
 KW transforming growth factor beta; TGF-beta.

OS Mus musculus.  
 XX

PH Key Location/Qualifiers  
 FT Cleavage-site 13-14  
 FT /label= Potential\_proteolytic\_cleavage\_site  
 FT cleavage-site 16-17  
 FT /label= Potential\_proteolytic\_cleavage\_site  
 FT /note= "cleavage generates mature protein"

PN WO9940181-A1.

XX 12-AUG-1999.

PD XX 05-FEB-1999; 99WO-US02511.

PR 28-JUL-1998; 98US-0124180.  
 PR 05-FEB-1998; 98US-0019070.  
 XX (YUJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
 XX PI Lee S, McPherron AC;  
 XX DR WPI; 1999-094289/41.  
 XX N-PSB; AA206446.

PT New differentiation factor useful for treating neurodegenerative  
 PT diseases  
 XX PS Example 2: Fig 2a; 138pp; English.

CC This is the amino acid sequence of the C-terminal region of the GDF-8  
 CC precursor protein. The predicted GDF-8 sequence contains two potential  
 CC proteolytic processing sites.  
 CC Cleavage of the precursor at the second of these sites would generate  
 CC a mature C terminal fragment 109 amino acids in length with a predicted  
 CC molecular weight of 12,400.  
 CC GDF-8 has been shown to result in increased bone and muscle mass (such  
 CC as ribs) when expressed in reduced amounts. GDF-8 minus transgenic  
 CC animals and forms of animal feed that can inhibit/reduce production of  
 CC GDF-8 are of commercial interest.  
 CC GDF-8 expression may also have a role in the therapy of abnormal growth  
 CC of muscle, bone or adipose tissue. A GDF-8 monoclonal antibody, GDF-8  
 CC antisense molecule or dominant negative polypeptide could be used with  
 CC foetal or adult muscle cells, bone cells or progenitor cells. These  
 CC agents can be administered to a patient suffering from a disorder such  
 CC as muscle wasting disease, neuro muscular disorder, muscle atrophy,  
 CC osteoporosis, bone degenerative diseases, obesity or other adipocyte  
 CC cell disorders, and aging for example.  
 XX SQ Sequence 126 AA;

Query Match 99.0%; Score 622; DB 20; Length 126;  
 Best Local Similarity 99.1%; Pred. No. 1; 6e-59; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DRGLCDEHSTESRCRCPYPLTVDFEARFQWDMWIAPKRYKANYCSGCECFVFLQKYPTHL 60  
 Db 18 df91dcdehstesrcrccrypltvdfefagfdwjiapkrykanycsgecefvlqkyphthl 77

Oy 61 VHQANPRGSAGCCTPLMSPINMLYFNGKQOIYKRYKIPAMVDRGCS 109  
 Db 78 vhqanprgsagcctplkmspinmlyfngkeqilqykipamvdrqcs 126

RESULT 5  
 AAB73182

ID AAB73182 standard; Protein: 126 AA.

XX AC AAB73182;  
 XX DT 11-MAY-2001 (first entry)

XX DE Murine GDF-8 #1.

XX Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia;  
 KW neurodegenerative disease; amyotrophic lateral sclerosis; obesity;  
 KW muscular dystrophy; musculodystrophic disease; tissue repair;  
 KW muscle wasting disease; neuromuscular disorder; spinal cord injury;  
 KW traumatic injury; congestive obstructive pulmonary disease.  
 OS Mus sp.  
 XX PN WO200112777-A2.  
 XX PD 22-FEB-2001.  
 XX

XX 17-AUG-2000; 2000WO-US22884.



FT Misc-difference 124  
 FT /note= "Cys-124 may be substituted by Ser to avoid  
 FT disulfide bond formation"  
 FT Misc-difference 141-142  
 FT /note= "optionally replaced by Glu-Gly"  
 PN WO200105820-A2.  
 XX PD 25-JAN-2001.  
 XX PR 20-JUL-2000; 2000WO-DK00413.  
 XX PR 20-JUL-1999; 99DK-0001014.  
 XX PR 26-JUL-1999; 99US-0145275.  
 PA (MEBI-) M & E BIOTECH AS.  
 XX Halkier T, Mouritsen S, Klyshner S;  
 DR WPI; 2001-112680/12.  
 XX DR WPI; 2001-112680/12.  
 XX PT Increasing the muscle mass of animals used in meat production by down  
 PT regulating growth differentiation factor 8 (GDF-8) activity in the  
 animal through induction of anti-GDF-8 antibody production  
 XX Example 1; Page 107-108; 110pp; English.  
 XX The present sequence is that of Autovac construct GDF-8 ext,  
 CC which consists of the C-terminal 160 amino acids of human growth  
 CC differentiation factor 8 (GDF-8, see AAF20131) with residues 16-36  
 CC substituted by the promiscuous tetanus toxin T-cell epitope P30 (see  
 CC AAB20144) and residues 37-51 substituted by tetanus toxin T-cell  
 CC epitope P2 (see AAB20143). It is an object of the invention to  
 CC produce a recombinant therapeutic vaccine that is capable of effecting  
 CC down-regulation of GDF-8 in order to increase the muscle growth  
 CC rate of farm animals. The vaccines (see AAB20145-53) are capable  
 CC of breaking autoimmunity against autologous GDF-8. They comprise  
 CC the C-terminal portion of human GDF-8 in which a portion of the  
 CC native sequence is replaced by a T-cell epitope such as P30, with  
 CC minimal disturbance of the authentic 3-dimensional structure of  
 CC the protein. Nucleic acids encoding the GDF-8 variants can be used  
 CC for genetic immunisation of the animals. Down-regulation of GDF-8  
 CC activity can increase muscle mass by up to at least 45% in cattle,  
 CC pigs and poultry used for meat production, reducing the need for  
 CC antibiotic feed-additives. Anti-GDF-8 vaccines can be used to  
 CC treat human diseases such as cancer cachexia where muscle atrophy is  
 CC pronounced and for patients suffering from acute and chronic heart  
 XX failure.  
 SQ Sequence 160 AA;  
 Query Match 99.0%; Score 622; DB 22; Length 160;  
 Best Local Similarity 99.1%; Pred. No. 2e-59; 0; Mismatches 108; Conservative 0; Indels 0; Gaps 0;  
 Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DRGLDDEHSTESRCRCRYPTVDFEAGWDMTIAPKRYKANYCSCGCEFPVILQKYPHTHL 60  
 DB 52 dfgldcdehstesrcrccryptvdfafeqgdwiaiapkrykanycsgcecfvflqkyphthl 111  
 QY 61 VHQANPRGSGAGPCCPTLMSDINMLVNGKQIYKTPKIPKANVDRGCS 109  
 DB 112 vhqanprgsgagpccptkmspimlyfnqkeqiygkipamvdrccgs 160  
 SQ Sequence 226 AA;  
 Query Match 99.0%; Score 622; DB 22; Length 226;  
 Best Local Similarity 99.1%; Pred. No. 2e-59; 0; Mismatches 108; Conservative 0; Indels 0; Gaps 0;  
 Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DFGLCDCEHSTESRCRCRYPTVDFEAGWDMTIAPKRYKANYCSCGCEFPVILQKYPHTHL 60  
 DB 118 dfgldcdehstesrcrccryptvdfafeqgdwiaiapkrykanycsgcecfvflqkyphthl 177  
 QY 61 VHQANPRGSGAGPCCPTLMSDINMLVNGKQIYKTPKIPKANVDRGCS 109  
 DB 178 vhqanprgsgagpccptkmspimlyfnqkeqiygkipamvdrccgs 226  
 SQ Sequence 254 AA;  
 RESULT 9  
 AAB20152  
 ID AAB20152 standard; Protein: 254 AA.  
 XX AC AAB20152;  
 XX DT 30-APR-2001 (first entry)  
 XX DE Growth differentiation factor 8 Autovac construct GDF-8 dimer.  
 XX KW Growth differentiation factor 8; GDF-8; myostatin; tetanus toxin;  
 DE Chicken GDF-8.  
 XX KW Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia;  
 KW neurodegenerative disease; amyotrophic lateral sclerosis; obesity;  
 KW muscular dystrophy; musculodystrophy; musculodystrophy disease; tissue repair;  
 KW traumatic injury; congestive obstructive pulmonary disease.  
 XX OS Gallus gallus.  
 XX PN WO200112777-A2.  
 XX PD 22-FEB-2001.  
 XX PR 17-AUG-2000; 2000WO-US22884.  
 XX PR 19-AUG-1999; 99US-0378238.  
 XX PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
 XX PI Lee S, McPherron AC;  
 DR WPI; 2001-211209/21.  
 XX N PSDB; AAF3554.  
 XX PS New substantially purified growth differentiation factor-8 polypeptide,  
 PT useful for treating muscle wasting disease, obesity, muscular  
 PT dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome  
 XX and cachexia.  
 XX Example 9; Fig 2; 124pp; English.  
 XX The present invention relates to growth differentiation factor-8 (GDF-8)  
 CC coding sequences and proteins. The present sequence is a GDF-8 protein,  
 CC which was isolated in the present invention. GDF-8 is useful for treating  
 CC neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and  
 CC muscular dystrophy), musculodystrophic diseases or in tissue repair due  
 CC to trauma, obesity and disorders relative to abnormal proliferation of  
 CC adipocytes. GDF-8 is also useful for treating malignancies of the various  
 CC organ systems, particularly cells in muscle or adipose tissues and in  
 CC gene therapy for the treatment of cell proliferative or immunological  
 CC diseases mediated by GDF-8. In addition, GDF-8 is also useful for  
 CC treating muscle wasting disease, neuromuscular disorder, spinal cord  
 CC injury, traumatic injury, congestive obstructive pulmonary disease  
 CC (COPD), AIDS or cachexia.  
 XX RESULT 9  
 AAB20152  
 ID AAB20152 standard; Protein: 254 AA.  
 XX AC AAB20152;  
 XX DT 30-APR-2001 (first entry)  
 XX DE Growth differentiation factor 8 Autovac construct GDF-8 dimer.  
 XX KW Growth differentiation factor 8; GDF-8; myostatin; tetanus toxin;

W T-cell epitope; down-regulation; vaccine; muscle; meat; cachexia;  
cardiant; human; mutant; murein.  
X Chimeric - Homo sapiens.  
S Chimeric - Clostridium tetani.  
Contractile

Region	1..109	Location/Qualifiers
Region	/note=" 109 C-terminal residues of human GDF-8 "	
Region	110..124	
Region	/note=" tetanus toxoid P2 epitope "	
Region	125..145	
Region	/note=" "tetanus toxoid p30 epitope"	
Region	146..254	
Misc-difference	90..91	/note=" 109 C-terminal residues of human GDF-8 "
Misc-difference	/note=" "optionally replaced by Glu-Gly"	
Misc-difference	235..236	
Misc-difference	/note=" "optionally replaced by Glu-Gly"	

AAB20132	standard; protein; 362 AA.
ID	
XX	
AC	
XX	
DT	30-APR-2001 (first entry)
XX	
DE	Turkey growth differentiation factor 8.
XX	
KW	Growth differentiation factor 8; GDF-8; myostatin; down-regulation;
KW	vaccine; muscle; meat; cachexia; cardiant; turkey.
XX	
OS	<i>Meleagris gallopavo</i> .
XX	

PD 25-JAN-2001.  
XX  
PP 20-JUL-2000; 2000WO-DK00413.  
XX  
PR 20-JUL-1999; 99DK-0001014.  
PR 26-JUL-1999; 99US-0145275.  
XX  
PA (MEBI-) M & BIOTECH AS.  
XX  
PT Halkier T, Mouritsen S, Klysner S;  
XX  
DR WPI; 2001-112680/12.

The present sequence is that of Autovac construct GDF-8 dimer comprising 2 copies of the 109-amino acid C-terminal region of human growth differentiation factor 8 (GDF-8, see Autovac<sup>TM</sup>).

Example 1; Page 76-78; 110pp; English.

PS  
XX  
CC  
CC  
CC  
CC  
XX

The present sequence is that of turkey growth differentiation factor 8 (GDF-8), also called myostatin. It is an object of the invention to produce a recombinant therapeutic vaccine capable of effecting animal through induction of anti-GDF-8 antibody production

connected through the P2 and P30 T-cell epitopes (see AAB20143-44) recombinant therapeutic vaccine that is capable of effecting down-regulation of GDF-8 in order to increase the muscle growth rate of farm animals. The vaccines (see AAB20145-53) are capable of breaking autotolerance against autologous GDF-8. They comprise the C-terminal portion of human GDF-8 in which a portion of the native sequence is replaced by a T-cell epitope such as P30, with minimal disturbance of the authentic 3-dimensional structure of the protein. Nucleic acids encoding the GDF-8 variants can be used for genetic immunization of the animals. Down-regulation of GDF-8 activity can increase muscle mass by up to at least 45% in cattle, pigs and poultry used for meat production, reducing the need for antibiotic feed-additives. Anti-GDF8 vaccines can be used to treat human diseases such as cancer cachexia where muscle atrophy is pronounced and for patients suffering from acute and chronic heart failure.

CC to produce a recombinant therapeutic vaccine capable of eliciting  
 CC down regulation of GDF-8 in order to increase the muscle growth  
 CC rate of farm animals. Variants of GDF-8 (see AAB20145-53) are  
 CC provided that are capable of breaking auto-tolerance against  
 CC autologous GDF-8. These comprise a C-terminal portion of human  
 CC GDF-8 in which a portion of the native sequence is replaced by a  
 CC C-terminal epitope such as the promiscuous tetanus toxin T-cell epitope  
 CC P2 or P30. Nucleic acids encoding the GDF-8 variants can be used  
 CC for genetic immunisation of the animals. Down-regulation of GDF-8  
 CC activity is used to increase muscle mass by up to at least 45%  
 CC in cattle, pigs and poultry used for meat production, reducing the  
 CC need for antibiotic feed-additives. Anti-GDF8 vaccines can be used  
 CC to treat human diseases such as cancer cachexia where muscle atrophy  
 CC is pronounced and for patients suffering from acute and chronic  
 CC heart failure.

Sequence . 254 AA

Query Match	99.0%	Score	622;	DB	22;	Length	362;
Best Local Similarity	99.1%	Pred.	No.	4	9.e-59		
Matches	108;	Conservative	0;	Mismatches	1;	Indels	0;

Query Match	99.0%	Score 622;	DB 22;	Length 254;
• Best Local Similarity	99.1%	Pred. NO.	3.3e-59	
Matches 108; Conservative	0	Mismatches	1	Indels 0
				Gaps 0

Db 3'4 vhdanprgsagcpctptkmspimlyfngkeqiykgipamvvdrccgs 362

RESULT 11

ID AAR63160

XX AAR63160 standard; Protein; 375 AA.

AC AAR63160;

XX DT 23-JUN-1995 (first entry)

XX DE Human growth differentiation factor-8 protein.

XX KW Growth differentiation factor-8; GDF-8; cell proliferation; adipocyte; obesity; transforming growth factor-beta.

XX SS Homo sapiens.

PA W09421681-A.

XX PD 29-SEP-1994.

XX PF 18-MAR-1994; 94WO-US030319.

PR 19-MAR-1993; 93US-0033923.

PA (UVJO ) UNIV JOHNS HOPKINS SCHOOL MED.

XX PI Lee S, McPherron AC;

XX DR WPI; 1994-316943/39.

DR Q-PSDB; Q76372.

XX PT New growth differentiation factor 8 - useful for treatment and diagnosis of cell proliferative disorders esp. of muscle.

XX PS Claim 3; Page 58; 84pp; English.

CC GDF-8 can be used to maintain cells before transplantation; to improve efficiency of cell fusion and to treat obesity or diseases related to abnormal adipocyte proliferation.

XX Sequence 375 AA;

Query Match 99.0%; Score 622; DB 15; Length 375;

Best Local Similarity 99.1%; Pred. No. 5.1e-59;

Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC DR GLDCDEHSTESRCCRYPLTVDFEAFCWDWITAPKRKYANCSGCEEFVFLQKYPHTL 60

QY 1 DFGLCDCEHSTESRCCRYPLTVDFEAFCWDWITAPKRKYANCSGCEEFVFLQKYPHTL 60

Db 267 dfglcdahstesrccrypltvdfafewgfdwiaipkrykanycsgeefvfliqkyphthl 326

QY 61 VHQANPRGSAGCPCTPTLSPIMLYFNGKEQIYKGIPAMVVDRCCGS 109

Db 327 vhdanprgsagcpctptkmspimlyfngkeqiykgipamvvdrccgs 375

RESULT 12

ID AAW69888

XX AAW69888 standard; Protein; 375 AA.

AC AAW69888;

XX DT 07-DEC-1998 (first entry)

XX DE Chicken growth differentiation factor-8.

XX KW Growth differentiation factor-8; GDF-8; chicken; transgenic animal; transforming growth factor-beta; muscle; meat; inhibitor; obesity; neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer; therapy.

XX SS Gallus sp.

OS Gallus sp.

XX FH Key location/Qualifiers

FT Cleavage-site 263..266

FT Protein 267..375

FT /label= Mat\_protein

XX PN W09833887-A1.

XX PD 06-AUG-1998.

XX PR 05-FEB-1998; 98WO-US02479.

XX PR 23-MAY-1997; 97US-0862245.

XX PR 07-FEB-1997; 97US-0795071.

XX PR 28-APR-1997; 97US-0847910.

XX PA (UVJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX PT Lee S, McPherron AC;

XX DR WPI; 1998-437444/37.

DR N-PSDB; AAV45819.

XX PT Transgenic animals with gene for growth differentiation factor-8 disrupted - have increased muscle and reduced cholesterol contents, also use of GDF-8 inhibitors for treating cancer, obesity, neuromuscular disease

XX PS Example 9; Fig 14c; 125pp; English.

CC This is the amino acid sequence of chicken growth differentiation factor-8 (GDF-8), a never member of the transforming growth factor-beta superfamily that appears to relate to various cell proliferative disorders, especially those involving muscle, nerve and adipose tissue. The sequence was deduced from a cDNA clone (see AAV45819) isolated from a skeletal muscle cDNA library. The invention provides novel mammalian and avian GDF-8 proteins (see AAV45819-92). A transgenic non-human animal is claimed in which GDF-8 expression is disrupted or interfered with. Also claimed are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb from those animals; (2) method for increasing muscle mass in animals by administering an antibody (Ab) that binds to GDF-8; (3) inhibiting the action of GDF-8 by treating foetal or adult muscle or progenitor cells with a GDF-8 inhibitor; (4) isolated nucleic acid encoding a GDF-8 protein truncated by loss of the C-terminal active fragment. The transgenic animals have increased muscle mass and for poultry reduced cholesterol contents. Method (3) is used to treat muscle wasting or neuromuscular diseases, muscular atrophy and aging, particularly muscular dystrophy, spinal cord or traumatic injuries, congestive or obstructive lung disease, AIDS and cachexia. Method (4) is used to treat cancer of muscle, connective tissue and bone, or obesity. Also (not claimed) GDF-8 can be used to maintain myoblasts intended for transplantation or to improve efficiency of fusion. Ab can be used to detect and quantify GDF-8 (particularly in muscle, for diagnosis or monitoring), also for immunotherapy and in vivo imaging.

CC Sequence 375 AA;

Query Match 99.0%; Score 622; DB 19; Length 375;

Best Local Similarity 99.1%; Pred. No. 5.1e-59;

Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC DR GLDCDEHSTESRCCRYPLTVDFEAFCWDWITAPKRKYANCSGCEEFVFLQKYPHTL 60

QY 1 DFGLCDCEHSTESRCCRYPLTVDFEAFCWDWITAPKRKYANCSGCEEFVFLQKYPHTL 60

Db 267 dfglcdahstesrccrypltvdfafewgfdwiaipkrykanycsgeefvfliqkyphthl 326

QY 61 VHQANPRGSAGCPCTPTLSPIMLYFNGKEQIYKGIPAMVVDRCCGS 109

Db 327 vhdanprgsagcpctptkmspimlyfngkeqiykgipamvvdrccgs 375

RESULT 13

XX AAW69891 standard; Protein: 375 AA.

ID AAW69891; XX

AC AAW69891; XX

DT 07-DEC-1998 (first entry) XX

DE Pig growth differentiation factor-8. XX

KW Growth differentiation factor-8; GDF-8; pig; transgenic animal; transforming growth factor-beta; muscle; meat; inhibitor; obesity; neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer; therapy. XX

OS Sus scrofa. XX

FH Key Location/Qualifiers XX

FT Cleavage-site 263..266 XX

FT protein 267..375 XX

FT /label= Mat\_protein W09833887-A1. XX

PD 06-AUG-1998. XX

PP 05-FEB-1998; 98WO-US02479. XX

XX 97US-0862445. XX

PR 23-MAY-1997; 97US-0795071. XX

PR 05-FEB-1997; 97US-0795071. XX

PR 28-APR-1997; 97US-0847910. XX

PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE. XX

PA Lee S, McPherron AC; XX

XX DR WPI; 1998-437444/37. XX

DR N-PSDB; AAV45822. XX

PT Transgenic animals with gene for growth differentiation factor-8 disrupted - have increased muscle and reduced cholesterol contents, also use of GDF-8 inhibitors for treating cancer, obesity, neuromuscular disease. XX

PT Example 9; Fig 14f; 125pp; English. XX

CC This is the amino acid sequence of the transforming growth factor-beta superfamily that appears to relate to various cell proliferative disorders, especially those involving muscle, nerve and adipose tissue. The sequence was deduced from a cDNA clone (see AAV5822) isolated from a skeletal muscle cDNA library. The invention provides novel mammalian and avian GDF-8 proteins (see AAW6983-92). A transgenic non-human animal is claimed in which GDF-8 expression is disrupted or interfered with. Also claimed are: (1) chicken or turkey eggs or meat; beef, milk, pork and lamb from these animal; (2) method for increasing muscle mass in animals by administering an antibody (Ab) that binds to GDF-8; (3) inhibiting the action of GDF-8 by treating foetal or adult muscle or progenitor cells with a GDF-8 inhibitor; (4) isolated nucleic acid encoding a GDF-8 protein truncated by loss of the C-terminal active fragment. The transgenic animals have increased muscle mass and for poultry reduced cholesterol contents. Method (3) is used to treat muscle wasting or neuromuscular diseases; muscular atrophy and aging, particularly muscular dystrophy, spinal cord or traumatic injuries, congestive or obstructive lung disease, AIDS and cachexia. Method (4) is used to treat cancer of muscle, connective tissue and bone, or obesity. Also (not claimed) GDF-8 can be used to maintain myoblasts intended for transplanting or to improve efficiency of fusion. Ab can be used to detect and quantify GDF-8 (particularly in muscle, for diagnosis or monitoring), also for immunotherapy and in vivo imaging. XX

RESULT 14

XX AAW69885 standard; Protein: 375 AA.

ID AAW69885; XX

AC AAW69885; XX

DT 07-DEC-1998 (first entry) XX

DE Human growth differentiation factor-8. XX

KW Growth differentiation factor-8; GDF-8; human; transgenic animal; transforming growth factor-beta; muscle; meat; inhibitor; obesity; neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer; therapy. XX

OS Homo sapiens. XX

FH Key Location/Qualifiers XX

FT Modified-site 71..73 XX

FT Cleavage-site /note= "Asn is N-glycosylated" XX

FT Protein 263..266 XX

FT /label= Mat\_protein W09833887-A1. XX

PD 06-AUG-1998. XX

PP 05-FEB-1998; 98WO-US02479. XX

PR 23-MAY-1997; 97US-0862445. XX

PR 05-FEB-1997; 97US-0795071. XX

PR 28-APR-1997; 97US-0847910. XX

PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE. XX

PA Lee S, McPherron AC; XX

XX DR WPI; 1998-437444/37. XX

DR N-PSDB; AAV45813. XX

PT Transgenic animals with gene for growth differentiation factor-8 disrupted - have increased muscle and reduced cholesterol contents, also use of GDF-8 inhibitors for treating cancer, obesity, neuromuscular disease. XX

PT Example 3; Fig 5c; 125pp; English. XX

CC This is the amino acid sequence of human growth differentiation factor-8 (GDF-8), a novel member of the transforming growth factor-beta superfamily that appears to relate to various cell proliferative disorders, especially those involving muscle, nerve and adipose tissue. The sequence was deduced from a cDNA clone (see AAV4810) isolated from a skeletal muscle cDNA library. The invention provides novel mammalian and avian GDF-8 proteins (see AAW6983-92). A transgenic non-human animal is claimed in which

CC GDF-8 expression is disrupted or interfered with. Also claimed

are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb

from: (2) method for increasing muscle mass in

animals by administering an antibody (Ab) that binds to GDF-8; (3)

inhibiting the action of GDF-8 by treating foetal or adult muscle

or progenitor cells with a GDF-8 inhibitor; (4) isolated nucleic

acid encoding a GDF-8 protein truncated by loss of the C-terminal

active fragment. The transgenic animals have increased muscle mass

and for poultry reduced cholesterol contents. Method (3) is used

to treat muscle wasting or neuromuscular disease, muscular atrophy

and aging, particularly muscular dystrophy, spinal cord or

traumatic injuries, congestive or obstructive lung disease, AIDS

and cachexia. Method (4) is used to treat cancer of muscle,

connective tissue and bone, or obesity. Also (not claimed) GDF-8

can be used to maintain myoblasts intended for transplanting or to

improve efficiency of fusion. Ab can be used to detect and

quantify GDF-8 (particularly in muscle, for diagnosis or monitoring),

also for immunotherapy and in vivo imaging.

SQ Sequence 375 AA;

Query Match 99.0%; Score 622; DB 19; Length 375;  
Best Local Similarity 99.1%; Pred. No. 5.1e-59; Matches 108; Conservative 0; Mismatches 1; Indels 0; gaps 0;  
Matches 108; Conservative 0; Mismatches 1; Indels 0; gaps 0;  
QY 1 DRGLDCDEHSTSRCCRYPLTVDFEARGDWIIAPKRYKANVCSCGCECFVFLQKYPTHL 60  
Db 267 dgldcdehstsrccrypltvdfeargdwiiapkrykancscgecfvflqkypthl 326  
QY 61 VHQANPRGSAGRCCTPLMSPINMLYFNGK50IYGKIPAMVDRGCS 109  
Db 327 vhqanprgsagpcctptkmspinmlyfngkeqiygkipamvdrqcs 375

RESULT 15  
AAW65460  
ID AAW65460 standard; Protein: 375 AA.  
XX  
AC AAW65460;  
XX  
DT 09-NOV-1998 (first entry)  
XX  
DE Human growth differentiation factor-8.  
XX  
W Growth differentiation factor-8; GDF-8; human.  
XS  
Homo sapiens.  
XX  
Key Location/Qualifiers  
PH  
FT Modified-site 71  
FT /note= "N'-glycosylated"  
FT Cleavage-site 263..266  
FT /note= "RXR proteolytic cleavage site"  
XX  
PN W09835019-A1.  
XX  
PR 06-FEB-1998; 98WO-US02310.  
XX  
PD 13-AUG-1998.  
XX  
PR 06-FEB-1998; 97US-0795671.  
XX  
PA (UYJO ) UNTV JOHNS HOPKINS SCHOOL MEDICINE.  
XX  
PI Lee S, McPherron AC;✉  
XX  
DR WPI; 1998-447217/38.

XX Transgenic animal growth differentiation factor-11 is inhibited - by  
PT insertion of transgene, also use of GDF-11 inhibitors for treating  
PT muscular wasting, neuromuscular disease, obesity

PS Example 3: Page 55-56; 89pp; English.

XX This is the amino acid sequence of human growth differentiation

factor-8 (GDF8). It shows a high degree of sequence homology

to the newly identified human growth differentiation factor-11

(GDF-11, see AAW65458). Alignment of the GDF-8 and GDF-11 sequences

reveals potential N-linked glycosylation signals and putative

proteolytic processing sites at analogous positions. The 2

sequences are related not only in the C-terminal region following

the putative cleavage site (90% amino acid sequence identity) but

also in the pro-region of the molecules (45% amino acid sequence

identity). Claimed transgenic animals in which GDF-11 production is

reduced produce higher than normal levels of muscle and are useful

in the food industry. GDF-11 polypeptides, polynucleotides and

antibodies can be used to modulate GDF-11 activity or gene

expression for treatment of cell proliferative disorders involving

XX muscle, nerve and adipose tissue.

SQ Sequence 375 AA;

Query Match 99.0%; Score 622; DB 19; Length 375;  
Best Local Similarity 99.1%; Pred. No. 5.1e-59; Matches 108; Conservative 0; Mismatches 1; Indels 0; gaps 0;  
Matches 108; Conservative 0; Mismatches 1; Indels 0; gaps 0;  
QY 1 DRGLDCDEHSTSRCCRYPLTVDFEARGDWIIAPKRYKANVCSCGCECFVFLQKYPTHL 60  
Db 267 dgldcdehstsrccrypltvdfeargdwiiapkrykancscgecfvflqkypthl 326  
QY 61 VHQANPRGSAGRCCTPLMSPINMLYFNGK50IYGKIPAMVDRGCS 109  
Db 327 vhqanprgsagpcctptkmspinmlyfngkeqiygkipamvdrqcs 375

Search completed: May 20, 2002, 09:21:47  
Job time: 82 sec





RESULT 2  
US-09-177-860A-6  
; Sequence 6, Application US/09177860A  
; Patent No. 6096506

GENERAL INFORMATION:  
APPLICANT: Huynh, Thanh  
APPLICANT: Lee, Se-Jin  
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN  
NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: US  
ZIP: 92121

COMPUTER READABLE FORM:  
COMPUTER: IBM Compatible  
COMPUTER SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/177,860A  
FILING DATE: 23-OCT-1998  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/525,596  
FILING DATE: 19-SEP-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Ph.D, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/075003

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 858-577-4565  
TELEFAX: 619-678-5099

INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 375 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-525-596B-14

Query Match 99 0%; Score 622; DB 3; Length 126;  
Best Local Similarity 99 1%; Pred. No. 3.3e-66; 1; Indels 0; Gaps 0;  
Matches 108; Conservative 0; Mismatches 1; Gaps 0;

QY 1 DFGLCDDEHSTESRCRYPTVDEAEGMDWILAPKRKANYCSECEVFQKPHL 60  
Db 18 DFGLCDDEHSTESRCRYPTVDEAEGMDWILAPKRKANYCSECEVFQKPHL 77

QY 61 VHQANPRGRSGAGPCCPTLMSPINMLYFNGKEQIYKGKIPAMVVRGCS 109  
Db 78 VHQANPRGRSGAGPCCPTKWSPINMLYFNGKEQIYKGKIPAMVVRGCS 126

RESULT 3  
US-08-525-596B-14  
; Sequence 5, Application US/08525596B  
; Patent No. 5827733  
; GENERAL INFORMATION:  
; APPLICANT: Huynh, Thanh  
; APPLICANT: Lee, Se-Jin

GENERAL INFORMATION:  
APPLICANT: LEE, SE-JIN  
APPLICANT: MCPHERRON, ALEXANDRA C.  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11  
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:  
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ  
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR  
CITY: LOS ANGELES  
STATE: CALIFORNIA  
COUNTRY: US  
ZIP: 90067

COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/765,875  
 FILING DATE: 08-SEP-1995  
 CLASSIFICATION: 5  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US/08/706,958  
 FILING DATE: 08-JUL-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: TUMARKIN PH.D., LISA A.  
 REGISTRATION NUMBER: P-38, 347  
 REFERENCE/DOCKET NUMBER: PD3641  
 TELECOMMUNICATION INFORMATION:  
 TELEFAX: 619/455-5100  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 375 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 IMMEDIATE SOURCE:  
 CLONE: GDF-8  
 FEATURE:  
 NAME/KEY: Protein  
 LOCATION: 1..375  
 ; US-08-795-671-5

Query Match 99.0%; Score 622; DB 2; Length 375;  
 Best Local Similarity 99.1%; Pred. No. 1.2e-65; Matches 108; Conservativeness 0; Mismatches 0; Indels 0; Gaps 0;  
 ; US-08-765-875-5

QY 1 DFGLCDCEHSTESTRCCRYPLTVDFEAFGDWITAPKRYKANCSGECFFVFLQKYPHTL 60  
 Db 267 DFGLCDCEHSTESTRCCRYPLTVDFEAFGDWITAPKRYKANCSGECFFVFLQKYPHTL 326  
 QY 61 VHQANPRGSAGPCCTPLMSPINMLYFNGKEQIYKIPAMVWDRCGCS 109  
 Db 327 VHQANPRGSAGPCCTPLMSPINMLYFNGKEQIYKIPAMVWDRCGCS 375

RESULT 5  
 US-08-765-671-5  
 ; Sequence 5, Application US/08795671  
 ; Patent No. 609834  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Se-Jin Lee and Alexandra McPheron  
 ; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Richardson P.C.  
 ; STREET: 4225 Executive Square, Suite 1400  
 ; CITY: La Jolla  
 ; STATE: California  
 ; COUNTRY: US  
 ; ZIP: 92121  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: DISKETTE  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows95  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/177,860A  
 ; FILING DATE: 23-OCT-1998  
 ; CLASSIFICATION: 424  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/525,596  
 ; FILING DATE: 19-SEP-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Haile, Ph.D., Lisa A.  
 ; REGISTRATION NUMBER: 38,347  
 ; REFERENCE/DOCKET NUMBER: 07265/075003  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 858-677-1456  
 ; FAX: 858-677-1455  
 ; INFORMATION FOR SEQ ID NO: 14:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 375 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; FRAGMENT TYPE: internal  
 ; US-09-177-860-14

RESULT 6  
 US-09-177-860A-14  
 ; Sequence 14, Application US/09177860A  
 ; Patent No. 6096506  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hoynh, Thanh  
 ; APPLICANT: Lee, Se-Jin  
 ; TITLE OF INVENTION: ANTIODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN  
 ; NUMBER OF SEQUENCES: 32  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Gray Cary Ware & Freidenrich LLP  
 ; STREET: 4335 Executive Drive, Suite 1600  
 ; CITY: San Diego  
 ; STATE: CA  
 ; COUNTRY: US  
 ; ZIP: 92121  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: DISKETTE  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows95  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/177,860A  
 ; FILING DATE: 23-OCT-1998  
 ; CLASSIFICATION: 424  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/525,596  
 ; FILING DATE: 19-SEP-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Haile, Ph.D., Lisa A.  
 ; REGISTRATION NUMBER: 38,347  
 ; REFERENCE/DOCKET NUMBER: 07265/075003  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 858-677-1456  
 ; FAX: 858-677-1455  
 ; INFORMATION FOR SEQ ID NO: 14:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 375 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; FRAGMENT TYPE: internal  
 ; US-09-177-860-14

RESULT 5  
 US-08-765-671-5  
 ; Sequence 5, Application US/08795671  
 ; Patent No. 609834  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Se-Jin Lee and Alexandra McPheron  
 ; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Richardson P.C.  
 ; STREET: 4225 Executive Square, Suite 1400  
 ; CITY: La Jolla  
 ; STATE: California  
 ; COUNTRY: US  
 ; ZIP: 92121  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: DISKETTE  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows95  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/177,860A  
 ; FILING DATE: 23-OCT-1998  
 ; CLASSIFICATION: 424  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/525,596  
 ; FILING DATE: 19-SEP-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Haile, Ph.D., Lisa A.  
 ; REGISTRATION NUMBER: 38,347  
 ; REFERENCE/DOCKET NUMBER: 07265/075003  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 858-677-1456  
 ; FAX: 858-677-1455  
 ; INFORMATION FOR SEQ ID NO: 14:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 375 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; FRAGMENT TYPE: internal  
 ; US-09-177-860-14

Query Match 99.0%; Score 622; DB 3; Length 375;

Best Local Similarity 99.1%; Pred. No. 1. 2e-65;

Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

US-09-177-860A-12  
Sequence 12, Application US/09177860A  
Patent No. 6036506

GENERAL INFORMATION:

APPLICANT: Huynh, Thanh

TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Gray Cary Ware &amp; Freidenrich LLP

STREET: 4365 Executive Drive, Suite 1600

CITY: San Diego

STATE: CA

COUNTRY: US

ZIP: 92121

COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/177,860A

FILING DATE: 23-OCT-1998

CLASSIFICATION: 424

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/525,596

FILING DATE: 19-SEP-1995

TELECOMMUNICATION INFORMATION:

TELEPHONE: 858-677-1456

TELEFAX: 858-677-1465

INFORMATION FOR SSO ID NO: 12:

SEQUENCE CHARACTERISTICS:

NAME: Hale, Ph.D. Lisa A.

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07265/075003

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-678-5099

TELEFAX: 619-678-5099

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 376 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-09-177-860A-12

RESULT 7

US-08-525-596B-12

Sequence 12, Application US/08525596B

Patent No. 5827733

GENERAL INFORMATION:

APPLICANT: Huynh, Thanh

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 AN

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish &amp; Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: US

ZIP: 92037

COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/525,596

FILING DATE: 19-SEP-1995

TELECOMMUNICATION INFORMATION:

TELEPHONE: 858-677-1456

TELEFAX: 858-677-1465

INFORMATION FOR SSO ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 376 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-09-177-860A-12

RESULT 9

US-08-891-789B-6

Sequence 6, Application US/08891789B

Patent No. 6103465

GENERAL INFORMATION:

APPLICANT: Grobet, Luc; Georges, Michel

TITLE OF INVENTION: Double-Muscling in Mammals

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: Blake, Cassels &amp; Graford

STREET: Box 25, Commerce Court West

CITY: Toronto

STATE: Ontario

COUNTRY: Canada

ZIP: M5L 1A9

COMPUTER READABLE FORM:

RESULT 8

US-08-525-596B-12

Query Match 99.0%; Score 622; DB 2; Length 376;

Best Local Similarity 99.1%; Pred. No. 1. 2e-65;

Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GENERAL INFORMATION:

APPLICANT: Lee, Se-Jin

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 AN

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Gray Cary Ware &amp; Freidenrich LLP

STREET: 4365 Executive Drive, Suite 1600

CITY: San Diego

STATE: CA

COUNTRY: US

ZIP: 92121

COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/177,860A

FILING DATE: 23-OCT-1998

CLASSIFICATION: 424

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/525,596

FILING DATE: 19-SEP-1995

TELECOMMUNICATION INFORMATION:

TELEPHONE: 858-677-1456

TELEFAX: 858-677-1465

INFORMATION FOR SSO ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 376 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-09-177-860A-12

RESULT 10

US-08-891-789B-6

Query Match 99.0%; Score 622; DB 2; Length 376;

Best Local Similarity 99.1%; Pred. No. 1. 2e-65;

Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GENERAL INFORMATION:

APPLICANT: Huynh, Thanh

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 AN

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish &amp; Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: US

ZIP: 92037

COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/177,860A

FILING DATE: 23-OCT-1998

CLASSIFICATION: 424

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/525,596

FILING DATE: 19-SEP-1995

TELECOMMUNICATION INFORMATION:

TELEPHONE: 858-677-1456

TELEFAX: 858-677-1465

INFORMATION FOR SSO ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 376 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-09-177-860A-12

RESULT 11

US-08-891-789B-6

Query Match 99.0%; Score 622; DB 2; Length 376;

Best Local Similarity 99.1%; Pred. No. 1. 2e-65;

Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GENERAL INFORMATION:

APPLICANT: Lee, Se-Jin

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 AN

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Gray Cary Ware &amp; Freidenrich LLP

STREET: 4365 Executive Drive, Suite 1600

CITY: San Diego

STATE: CA

COUNTRY: US

ZIP: 92121

COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/177,860A

FILING DATE: 23-OCT-1998

CLASSIFICATION: 424

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/525,596

FILING DATE: 19-SEP-1995

TELECOMMUNICATION INFORMATION:

TELEPHONE: 858-677-1456

TELEFAX: 858-677-1465

INFORMATION FOR SSO ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 376 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-09-177-860A-12

RESULT 12

US-08-891-789B-6

Query Match 99.0%; Score 622; DB 2; Length 376;

Best Local Similarity 99.1%; Pred. No. 1. 2e-65;

Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GENERAL INFORMATION:

APPLICANT: Huynh, Thanh

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 AN

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish &amp; Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: US

ZIP: 92037

COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/177,860A

FILING DATE: 23-OCT-1998

CLASSIFICATION: 424

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/525,596

FILING DATE: 19-SEP-1995

TELECOMMUNICATION INFORMATION:

TELEPHONE: 858-677-1456

TELEFAX: 858-677-1465

INFORMATION FOR SSO ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 376 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-09-177-860A-12

4 MEDIUM TYPE: diskette, 3 1/2 inch, 1.4 Mb storage  
 COMPUTER: COMPAQ, IBM PC compatible  
 OPERATING SYSTEM: MS-DOS 5.1  
 SOFTWARE: WORD PERFECT  
 CURRENT APPLICATION DATA:  
 FILING DATE: JULY 14, 1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hunt, John C.  
 REGISTRATION NUMBER: 36 424  
 REFERENCE/DOCKET NUMBER: 52836/00004  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (416) 863-4344  
 TELEFAX: (416) 863-2653  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 376 amino acids  
 TOPOLOGY: linear  
 STRANDEDNESS: single  
 TYPE: amino acid  
 ; US-08-891-789B-6

RESULT 10  
 Query Match 99.0%; Score 622; DB 3; Length 376;  
 Best Local Similarity 99.1%; Pred. No. 1.2e-65; Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DFGLCDDEHSTESRCRCPPLTVDFEARFQWDWITAPKRKYKANCSGECBFVFLQYPHTL 60  
 Db 267 DFGLCDDEHSTESRCRCPPLTVDFEARFQWDWITAPKRKYKANCSGECBFVFLQYPHTL 326  
 QY 61 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIYKGKIPAMVWDRCGCS 109  
 Db 328 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIYKGKIPAMVWDRCGCS 376

RESULT 11  
 US-08-525-596B-8  
 Sequence 8: Application US/08525596B  
 ; Patent No. 5827733  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Huynh, Thanh  
 ; APPLICANT: Lee, Se-Jin  
 ; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8  
 ; NUMBER OF SEQUENCES: 32  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Richardson P.C.  
 ; STREET: 4225 Executive Square, Suite 1400  
 ; CITY: La Jolla  
 ; STATE: CA  
 ; COUNTRY: US  
 ; ZIP: 92037  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows95  
 ; SOFTWARE: FastSQL for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/525, 596B  
 ; FILING DATE: 19-SEP-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US94/07762  
 ; FILING DATE: 03-JUL-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Wetherell, Jr., Ph.D., John R.  
 ; REGISTRATION NUMBER: 31,678  
 ; REFERENCE/DOCKET NUMBER: 07265/075001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 619-678-5070  
 ; TELEFAX: 619-678-5099  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 108 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; FRAGMENT TYPE: internal  
 ; US-08-525-596B-8

Query Match 97.3%; Score 611; DB 3; Length 375;  
 Best Local Similarity 97.2%; Pred. No. 2.4e-64; Matches 106; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DFGLCDDEHSTESRCRCPPLTVDFEARFQWDWITAPKRKYKANCSGECBFVFLQYPHTL 60  
 Db 267 DFGLCDDEHSTESRCRCPPLTVDFEARFQWDWITAPKRKYKANCSGECBFVFLQYPHTL 326  
 QY 61 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIYKGKIPAMVWDRCGCS 109  
 Db 327 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIYKGKIPAMVWDRCGCS 375

Query Match 97.3%; Score 583; DB 2; Length 108;  
 Best Local Similarity 99.0%; Pred. No. 1.1e-61; Matches 102; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DFGLCDDEHSTESRCRCPPLTVDFEARFQWDWITAPKRKYKANCSGECBFVFLQYPHTL 60  
 Db 6 DFGLCDDEHSTESRCRCPPLTVDFEARFQWDWITAPKRKYKANCSGECBFVFLQYPHTL 65  
 QY 61 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIYKGKIPAMV 103  
 Db 66 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIYKGKIPAMV 108

US-08-891-789B-2

RESULT 12  
 US-08-891-789B-2  
 Sequence 9: Application US/08891789B  
 ; Patent No. 5827733  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hunt, John C.  
 ; APPLICANT: Grobet, Luc; Georges, Michel  
 ; TITLE OF INVENTION: Double-Muscling in Mammals  
 ; NUMBER OF SEQUENCES: 52  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Blake, Cassels & Graydon  
 ; STREET: Box 25, Commerce Court West  
 ; CITY: Toronto  
 ; STATE: Ontario  
 ; ZIP: M5L 1A9  
 ; COUNTRY: Canada  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: MS-DOS 5.1  
 SOFTWARE: WORD PERFECT  
 CURRENT APPLICATION DATA:  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows95  
 SOFTWARE: FastSQL for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/525, 596B  
 FILING DATE: 19-SEP-1995  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US94/07762  
 FILING DATE: 03-JUL-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Wetherell, Jr., Ph.D., John R.  
 REGISTRATION NUMBER: 31,678  
 REFERENCE/DOCKET NUMBER: 07265/075001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-678-5070  
 TELEFAX: 619-678-5099  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 108 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 ; US-08-525-596B-8

Query Match 97.3%; Score 583; DB 2; Length 108;  
 Best Local Similarity 99.0%; Pred. No. 1.1e-61; Matches 102; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DFGLCDDEHSTESRCRCPPLTVDFEARFQWDWITAPKRKYKANCSGECBFVFLQYPHTL 60  
 Db 6 DFGLCDDEHSTESRCRCPPLTVDFEARFQWDWITAPKRKYKANCSGECBFVFLQYPHTL 65  
 QY 61 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIYKGKIPAMV 103  
 Db 66 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIYKGKIPAMV 108

US-08-891-789B-2

RESULT 12  
 US-09-177-860A-9  
 Sequence 8, Application US/09177860A  
 Patent No. 6096506  
 GENERAL INFORMATION:  
 APPLICANT: Huynh, Thanh  
 TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN  
 NUMBER OF SEQUENCES: 32  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Gray Cary Ware & Freidenrich LLP  
 STREET: 4365 Executive Drive, Suite 1600  
 CITY: San Diego  
 STATE: CA  
 COUNTRY: US  
 ZIP: 92121  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: Windows95  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/177,860A  
 FILING DATE: 23-OCT-1998  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/525,596  
 FILING DATE: 19-SEP-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Haile, Ph.D. Lisa A.  
 REGISTRATION NUMBER: 38,347  
 REFERENCE/DOCKET NUMBER: 07265/075003  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 858-677-1456  
 FAX: 858-677-1465  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 108 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-09-177-860A-9

Query Match 92.8%; Score 583; DB 3; Length 108;  
 Best Local Similarity 99.0%; Pred. No. 1.1e-61; Mismatches 0; Indels 1; Gaps 0;  
 Matches 102; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLDCDEHSTESRCRYPITVDFEAFGWMWIAPIKRYKANYCCECEVFQKYPHTL 60  
 6 DFGLDCDEHSTESTRCRYPITVDFEAFGWMWIAPIKRYKANYCSECEVFQKYPHTL 65

QY 61 VHQANPRGSAGPCPCTPLASPINMLYFNGEQIYGKIPAMV 103  
 66 VHQANPRGSAGPCPCTPLASPINMLYFNGEQIYGKIPAMV 108

Db. 78 VQANPRGSAGPCPCTPLASPINMLYFNGEQIYGKIPAMV 126

RESULT 13  
 US-08-247-907A-2  
 Sequence 2, Application US/08247907A  
 Patent No. 5539638  
 GENERAL INFORMATION:  
 APPLICANT: WOMNEY, John  
 APPLICANT: CELESTE, Anthony J.  
 TITLE OF INVENTION: BMP-11 COMPOSITIONS  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: GENETICS INSTITUTE, INC.  
 STREET: 87 CambridgePark Drive  
 CITY: Cambridge  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02140

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/452,772  
 FILING DATE: 30-MAY-1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/247,907  
 FILING DATE: 20-MAY-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: LAAR Severyn R.  
 REGISTRATION NUMBER: 32,618  
 REFERENCE/DOCKET NUMBER: G15205-CP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617 876-1170

RESULT 14  
 US-08-452-772-2  
 Sequence 2, Application US/08452772  
 Patent No. 5700911  
 GENERAL INFORMATION:  
 APPLICANT: WOMNEY, John  
 APPLICANT: CELESTE, Anthony J.  
 TITLE OF INVENTION: BMP-11 COMPOSITIONS  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: GENETICS INSTITUTE, INC.  
 STREET: 87 CambridgePark Drive  
 CITY: Cambridge  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02140

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/452,772  
 FILING DATE: 30-MAY-1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/247,907  
 FILING DATE: 20-MAY-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: LAAR Severyn R.  
 REGISTRATION NUMBER: 32,618  
 REFERENCE/DOCKET NUMBER: G15205-CP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617 876-1170

ZIP: 02140  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/247,907A  
 FILING DATE: May 20, 1994  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: LAZAR, Steven R.  
 REGISTRATION NUMBER: 32,618  
 REFERENCE/DOCKET NUMBER: G15205-A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617 876-1170  
 TELEFAX: 617 876-5851  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 126 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-247-907A-2

Query Match 91.4%; Score 574; DB 1; Length 126;  
 Best Local Similarity 89.0%; Pred. No. 1.5e-60; Mismatches 5; Indels 0; Gaps 0;  
 Matches 97; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DFGLDCDEHSTESRCRYPITVDFEAFGWMWIAPIKRYKANYCCECEVFQKYPHTL 60  
 Db 18 NLGLDCDEHSSESRCRYPITVDFEAFGWMWIAPIKRYKANYCSECEVFQKYPHTL 77

QY 61 VHQANPRGSAGPCPCTPLASPINMLYFNGEQIYGKIPAMV 109  
 Db. 78 VQANPRGSAGPCPCTPLASPINMLYFNGEQIYGKIPAMV 126

TELEFAX: 617 876-5851  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 126 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-452-772-2

Query Match 91.4%; Score 574; DB 1; Length 126;  
 Best Local Similarity 89.0%; Pred. No. 1; 5e-60;  
 Matches 97; Conservative 7; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 DFGLCDDEHSTESRCCRYPLTVDFEAFCGDWITAPKRKYKANCGSGCECFVFLQKYPITHL 60  
 OY 18 NLGLDCDBHSSBESRCCRYPLTVDFEAFCGDWITAPKRKYKANCGSGCECFVFLQKYPITHL 77  
 QY 61 VHQANPRGSAGPCCTPLMSPINMLYFNGKEQIYKGKIPAMVYDRCGCS 109  
 Db 78 VQOANPRGSAGPCCTPLMSPINMLYFNDKQOQIYKGKIPAMVYDRCGCS 126

RESULT 15

US-08-765-875-4

Sequence 4, Application US/08765875

Patent No. 5914234

GENERAL INFORMATION

APPLICANT: LEE, SE-JIN

APPLICANT: MCPHERRON, ALEXANDRA C.

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: SPINSLEY HORN JUBAS & LUBITZ  
STREET: 1880 CENTURY PARK EAST, FIFTH FLOORCITY: LOS ANGELES  
STATE: CALIFORNIA  
COUNTRY: US  
ZIP: 90067

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/765,875

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/706,958

FILING DATE:

APPLICATION NUMBER: US/08/272,763

FILING DATE: 08-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: TUMARKIN PH.D., LISA A.

REGISTRATION NUMBER: P-38,347

REFERENCE/DOCKET NUMBER: PD3641

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/455-5100

TELEFAX: 619/455-5110

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 126 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-765-875-4

Query Match 91.4%; Score 574; DB 2; Length 126;  
 Best Local Similarity 89.0%; Pred. No. 1.5e-60;  
 Matches 97; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DFGLCDDEHSTESRCCRYPLTVDFEAFCGDWITAPKRKYKANCGSGCECFVFLQKYPITHL 60  
 Db 18 NLGLDCDBHSSBESRCCRYPLTVDFEAFCGDWITAPKRKYKANCGSGCECFVFLQKYPITHL 77  
 QY 61 VHQANPRGSAGPCCTPLMSPINMLYFNGKEQIYKGKIPAMVYDRCGCS 109  
 Db 78 VQOANPRGSAGPCCTPLMSPINMLYFNDKQOQIYKGKIPAMVYDRCGCS 126

Search completed: May 20, 2002, 09:20:47  
 Job time: 22 sec

Mon May 20 09:12:34 2002

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